

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 17:50:05 ; Search time 226 Seconds
(without alignments)
8319.877 Million cell updates/sec

Title: US-09-835-976B-15
Perfect score: 4260
Sequence: 1 tgaatagaagtattcttagt.....aaaaaaaaaaaaaaaaaaaaa 4260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1648.4	38.7	3722	4	US-09-016-434-1129
2	514.4	12.1	2384	1	US-07-688-352C-27
3	514.4	12.1	2384	2	US-08-474-379C-27
4	514.4	12.1	2384	3	US-09-146-249A-27
5	514.4	12.1	2384	3	US-08-206-188B-27
6	514.4	12.1	2384	5	PCT-US91-02714-25
7	226	5.3	227	4	US-09-016-434-294
8	136.4	3.2	254	4	US-09-016-434-464
9	123.4	2.9	235	4	US-09-016-434-614
10	116	2.7	231	4	US-09-016-434-475
11	110.2	2.6	236	4	US-09-016-434-371
12	92.6	2.2	4098	4	US-09-268-866-1
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16	40.6	1.0	2447	4	US-09-014-969-14
17	39.4	0.9	2271	4	US-09-205-258-243
18	39.4	0.9	2276	4	US-09-205-258-183
19	39.2	0.9	289	3	US-09-007-005-17
20	39.2	0.9	289	3	US-09-244-796-17
21	38.8	0.9	441	4	US-09-601-537-10
22	38.8	0.9	1332	2	US-09-057-762-1
23	38.8	0.9	1332	3	US-08-326-119A-1
24	38.8	0.9	1493	6	5340934-5
25	38.8	0.9	4121	4	US-09-601-537-9
26	38.6	0.9	251	3	US-09-221-298-23
27	38.4	0.9	3527	2	US-08-909-965C-7
					Sequence 1129, Ap
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 25, Appl
					Sequence 294, App
					Sequence 464, App
					Sequence 614, App
					Sequence 475, App
					Sequence 371, App
					Sequence 1, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 183, App
					Sequence 17, Appl
					Sequence 10, Appl
					Sequence 1, Appl
					Patent No. 5340934
					Sequence 9, Appl
					Sequence 23, Appl
					Sequence 7, Appl

28	38	0.9	208	1	US-08-686-878A-37	Sequence 37, Appl
29	38	0.9	208	4	US-09-175-928-37	Sequence 37, Appl
30	37.8	0.9	1693	2	US-08-487-113D-118	Sequence 118, App
31	37.8	0.9	1693	3	US-08-720-420A-118	Sequence 118, App
32	37.8	0.9	2296	3	US-08-496-841C-137	Sequence 137, App
33	37.8	0.9	2634	2	US-08-818-514-1	Sequence 1, Appl
34	37.8	0.9	2634	2	US-08-818-514-2	Sequence 2, Appl
35	37.8	0.9	2634	3	US-09-115-934A-1	Sequence 1, Appl
36	37.8	0.9	2634	3	US-09-115-934A-2	Sequence 2, Appl
37	37.8	0.9	2634	4	US-09-611-175-1	Sequence 1, Appl
38	37.8	0.9	2634	4	US-09-611-175-2	Sequence 2, Appl
39	37.4	0.9	1249	4	US-09-461-325-128	Sequence 128, App
40	37.4	0.9	1260	4	US-09-461-325-93	Sequence 93, Appl
41	37	0.9	2589	3	US-08-569-749-1	Sequence 1, Appl
42	37	0.9	2589	5	PCT-US96-12860-1	Sequence 1, Appl
43	36.8	0.9	1641	1	US-08-300-903A-8	Sequence 8, Appl
44	36.8	0.9	1641	4	US-08-988-197-8	Sequence 8, Appl
45	36.8	0.9	2434	4	US-09-489-847-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1129
; Sequence 1129, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1399211
US-09-016-434-1129

Query Match 38.7%; Score 1648.4; DB 4; Length 3722;
Best Local Similarity 71.1%; Pred. No. 0;

Matches 2196; Conservative 0; Mismatches 888; Indels 6; Gaps 1;			
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Qy	596	GAAGGTGCTTCCCTCCTCAACCGCATGGCCAAATACACTAATCTGACTCAAGGAGCAAA	655
Db	286	AAAGGTATCGTCTCTCTGGGAAAGCTCGTAGCTACACCACTCAACCAGGGGCCAA	345
Qy	656	GAACAATGAAGAGGAGCAAAAACATCCTGAAGGGGAAAAGAGCCCAACAAAGACCCCA	715
Db	346	AGAGCATGAGGAGGCCGAGGTGGGAGGGCCACCCCGCGAGGGCAGCGAGGCCACCCAG	405
Qy	716	AATGGGTACTCTCATGGGTGTCTACTCCCATGTCTACAAATATTTTGGAGTATCCT	775
Db	406	CATGGGCACCTCATGGGGGTGTACCTGCCCTGCCCTGCAGAAATATCTTTGGGGTATCCT	465
Qy	776	TTTTTTTACGCTTACATGGGTGGTGGGCACAGCTGGAGTCTTTCAGGGCTTTTGGCAATTGT	835
Db	466	CTTCTCGCGCTGACCTGGATGGTGGGCACAGAGTGTCTACAGGCCCTCTCATCGT	525
Qy	836	CTTATCTGCTGCTGTCTACAAATGTTGACTGTATCTCCATGAGTGCCATTTGCCACTAA	895
Db	526	GCTTATCTGCTGTGTGTACCTGCTGACGGCCATCTCCATGAGTGCCATCGCCACCAA	585
Qy	896	TGGAGTGGTCCAGCTGGGGGCTCATCTTTATGATTTCCGGGCACCTGGGCCAGAGTT	955
Db	586	CGGTGTGGTTCAGCTGGGGGCTCTATTTTCATGATCTCTCGTTCACTGGGGCCAGAAAT	645
Qy	956	TGTTGGGGTGTGGGCTCTGCTTTTATCTTGTTACCAATTTGAGAGCCATGTACAT	1015
Db	646	TGGAGTGTCTGGGCTGTGCTTCTACCTGGGAACAATTCGACGACGCCATGTACAT	705
Qy	1016	CTTGTGTCATGAAATCTTTCTGTCTATATGTCCTGATATGTCCTGAGTGCCATCTTTACAG	1075
Db	706	CTGGGGGCGCATCGAGATCTTGTGACCTACATTTGCCACACAGCTGCCATTTTTTACCC	765
Qy	1076	TGATGAGGCACCTCAAGGAATCAGCAGCCATGCTTAATACATCGCTGTCTAGGCACAGC	1135
Db	766	ATCGGTGTCTATGACACGCTGGAATGCCACTTTTGAACAATATGCGTGTATGGGACCAT	825
Qy	1136	TTTCTTGGTCTTATGGTATTTAGTGTATTTATTCGGCGTACGCTATGTGAAACAAGTTTGC	1195
Db	826	TTTCTGACCTTCATGACCTGTGTGTGTGTGGGGTCAAGTATGTGAACAATTTGC	885
Qy	1196	CTCAATTTTCTGGCCTGTGTCTATGTGTCATCTTTGGCCATCTATGCTGGAGCCATCAA	1255
Db	886	CTCGCTCTTCTGGCCTGTGTATCATCTCCATCTCTCCATCTATGCTGGGGGCATAA	945
Qy	1256	GTCTTCTTTTGTCTCCACACTTCCGGGTCTGCATGCTGGGTAAACCGCACTTTTTCATC	1315
Db	946	GTCTATTTTGAACCTCCCGTGTTCCTGGTATGATGCTGGGGAACAGGACCTGTGCCG	1005
Qy	1316	AAGACACATTTGCTTGTCTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAA	1375
Db	1006	GGACCAAGTTTATCATCTGTGCCAAGACAGCTGTAGTGGACATGACAGTGGCCACCA	1065
Qy	1376	GTTATGGGATCTTCTGTAACTCGAGTCAATTTTTTCAATGCCACCTGTGATGAATATT	1435
Db	1066	GCTATGGAGTTTCTTCTGACACAGCCCAACCTTACGACCGACTCTCTGTGACCCCTACTT	1125
Qy	1436	TGTTCAATAAGCTCATCTCAATCCAGGCATCTCTGGATTGGCTAGTGGTATATTAC	1495
Db	1126	CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGCTGGTGTGTCCA	1185
Qy	1496	AGAAATCTTTGGAGTAAATTACCTACCAAGGAGAGATCATCGAAAAGCCTTCAGCCAA	1555
Db	1186	GGAACACCTGTGAGCGCCTACCTGGNAGAGGTGACATCGTGAGAGCATGGGTGCC	1245
Qy	1556	ATCTTCTGATGCTTTAGGAGCTTAA-----CCATGAATATGTTCTTTTGACATCAC	1609
Db	1246	CTCCGAGATGCCCCGAGCCTGAAGAGAGAGCCTGCTCTGTACGTGGTGGTGCATCGC	1305

Qy	1610	CACCTCTTCACTGCTTCTGGTGGAAATCTTCTTTCCCTCTGTTACAGGTATCATGGCTGG	1669
Db	1306	CACATCTTTACCCTGTGGTGGCACTCTTCTTCCCTTCTGTAAACAGCATCATGGCTGG	1365
Qy	1670	ATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAAAGTCTATTTCCGATTTGATATCTCT	1729
Db	1366	CTCAACCGCTCTGGGACCTTCTGTAGCGCCAGAAAGTCTATCTCTGTGGGAGCAATCTCT	1425
Qy	1730	TGCCATCTGACACCTCTTCTTTTATTTAAAGCAATGTTGCTCTTTTCTGGTGCATGAT	1789
Db	1426	GGCCATCATTAACAATTTCCCTCGTGTACTTCAGCAGTGTGGTCTCTTTGGTGGCTGCAT	1485
Qy	1790	TGAAGGGTGTCTCTCAGAGACAAATTCGGTGTGCTGTGAAAGGTAAATTTGGTGGTAGG	1849
Db	1486	TGAGGGTGTGGTCTCTCGGACAGATATGGCGATGGTGTGACAGGAACTTTGGTGGTGGG	1545
Qy	1850	CACCTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGGCTCTTCTTTTCAACATGTGG	1909
Db	1546	CACACTGGCTGGCTTCACTGGTCTATCGGCTCTCTCTTTTCAACGTGTGG	1605
Qy	1910	GGCTGGATTCAGAGCCTCAGAGTGCACGAGGCTGCTACAAGCTATTTGCCAAGGATAA	1969
Db	1606	CGCTGGCTCCAGAGCCTCAGAGGGGACCAACGCTATTTGAGGCCATTTGCCAAGGACAA	1665
Qy	1970	CATCATACCGTTCTGAGGGTTTTGGCCACAGCAAAAGCCAAATGGGAAACCTACTGGGC	2029
Db	1666	CATCATCCCTTCTCTGGGTGTTTGGCCACGGGAAGTGAATGGTGAACCCACATGGGC	1725
Qy	2030	TTTATCTTAACTCTGCTGCCATTTGAGAGCTTTGGAATACTCAATGCTCTCTCTGGATCTTGT	2089
Db	1726	ACTCTCTGACGCACTCATCGCGAGCTGGGCATCTCATCGCTCTCTCTCGACATGGT	1785
Qy	2090	GGCCCCATCTTTTCCATGTTTCTCATGTGTACTCTCTTCTTAACTTTGGCATGTC	2149
Db	1786	GGCCCCATCTTATCCATGTTCTTCTGATGTGCTACCTGTTCGTGAACCTCGCTGTGC	1845
Qy	2150	CTTGCAAACTTACTTCGAACACCACTGGAGACCCCGATTTCCGCTACTACCATTTGGGC	2209
Db	1846	GGTGAGACACTCTCTGAGGACCCCACTGGCGCCCGGTTCAAGTACTATCACTGGGC	1905
Qy	2210	CTTTCTTTCATGGGAATGAGTATCTGTGGCTCTGATGTTCAITTTCTTCTCTGGTATTA	2269
Db	1906	GCTGTCTTCTGGCATGAGTCTCTGCTGGCTTATGTTGTCTCTCTCTCTGCTACTA	1965
Qy	2270	TGCCATTTGACCCATGTAATAGTGTATGATCTACAAGTACATTTGAATACCAAGGAGC	2329
Db	1966	TGCCCTGGTGCCCATGCTCATCGCGGCATGATCTTACAAATACATCGAGTACCAAGGGGC	2025
Qy	2330	TGAGAAAGATGGGTGATGTTATCCGTGGCTGTCTCTCAGTGCAGCCCGGTTTGTCTTT	2389
Db	2026	TGAGNAGAGTGGGTGACGGGATCCGAGGCTGTCTCTGAGCGCTGCCCGCTAGCGCT	2085
Qy	2390	GCTTCGATTTGAGGAGGACCTCCACACACTTAAAACTGGAGGCTCAGTGTCTTGTATT	2449
Db	2086	GTTGGCGCTGGAGAGGGGCTCTCTCACACAAGAACTGGCGGCGCAGCTGTGTGTCT	2145
Qy	2450	ACTGAACTAGATGAAAGCTTACATGTCAAGCATCTCGCTCTCCTCCTTTCCTCACA	2509
Db	2146	GCTGAAGCTGACGAGGACCTCCAGTGAATCCCGGGCTCTCTCCTTTCCTCTCCCA	2205
Qy	2510	GCTCAAGCAGAAAAGGTTTCACTATTGTGGGCTCTCTCATCTGTGGGAACTTCTCTAGA	2569
Db	2206	GCTCAAGCTGGCAAGGCTGACCAATTTGTTGTTCTCTCATCCAGGGGAGCTTCTTGA	2265
Qy	2570	GAACTACCGTGAAGCTTTAGTGTGACAGACCAATAAGCACTTAATGGAGGACAGAA	2629
Db	2266	GAGCTATGGCGAGGCTCAGGCGCGCAGACCACTCAAGAACATGATGGAATTTGAGAA	2325
Qy	2630	GTTAAAGGATTTCTCCAGCTGGTGGCGCCCAAGCTGAGAGAGGCACTTTTCCACCT	2689
Db	2326	GGTGAAGGGCTTCTCCAGGTGGTGGCCAGCAAGGTGGGGAGGGGCTGGCCACCT	2385

D _b	S97	CGGTGTTCTCAGCTGGGGGCCTTAATTTCAATCATCTCTCTGTTCACTGGGGCCAGAATT	556
Q _y	956	TGTTGGGGCTGTTGGCCCTCTGCTTTTTATCTTGGTACCACATTTTGACAGGCCATGTACAT	1015
D _b	657	TGGAGGTGCTGTGGGCTGTGCTTCTACCTGGGAACAACATTCGACAGGCCATGTACAT	716
Q _y	1016	CCTTGGTGCCATTGAAATCTTTCTGTGCTATATCTGTCCTCCCGAGCTGCCATCTTTACAG	1075
D _b	717	CCTGGGGGCCATCGAGATCTTGCTGACCTACATTGCCCCACAGCTGCCATTTTTTACCC	776
Q _y	1076	TGATGCGCACTCAAGGAATCACGAGCCATGCTAAATAACATCGCTGTCTACGGSCACAGC	1135
D _b	777	ATCGGGTCTCATGACACGTCGAATGCCACTTTGAACAATATCGGTGTGTATGGGACCAT	836
Q _y	1136	TTTCTTGGTCTTATGGTATTAGTGGTATTTATCGCGTAGCGTATGTGAACAAGTTTGC	1195
D _b	837	TTTCTGGCTTCATGACCCCTGGTGGTGTGTGGGGTCAAATATGTGAACAAATTTGC	896
Q _y	1196	CTCANTTTTCTGGCCGTGTCTATTGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAA	1255
D _b	897	CTCGCTTCTCTGGCCGTGTGATCATCTCCATCCTCTCCATCTATGCTGGGGGCATAA	956
Q _y	1256	GTCCTCTTTTGTCTCTCCACACTTCCCGGTCTGCATGCTGGGTAAACGCACTCTTTTCATC	1315
D _b	957	GTCTATATTGACCTCCCGTGTTCGGGTATGATGCTGGGCAACAGGACCTGTGCCG	1016
Q _y	1316	AAGACATATTGACGTTTGTCTTAAGAACAAAGGAAATTAACAACATGACAGTCCCACAA	1375
D _b	1017	GGACCA GTTTGACATCTGTGCCAAGACAGCTGTAGTGGA CAATGAGACAGTGGCCACCOA	1076
Q _y	1376	GTTATGGGGATTCTTCTGTAACTCGAGTCAATTTTTC AATGCCACCTGTGATGAATACTT	1435
D _b	1077	GCTATGAGATTCTTCTGCCACAGCCCAACCTTACGACGAGTCTCTGTGACCCCTACTT	1136
Q _y	1436	TGTTCAACAATAACGTCACTTCAATCCAGGGCATTCCTGGATTGGCTAGTGGTATAATTAC	1495
D _b	1137	CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGCTGGTGTCTCCA	1196
Q _y	1496	AGAAATCTTTGGAGTAATTA CTCTCAAGGAGGAGATCATCGAAAAGCCTTCAGCCAA	1555
D _b	1197	GGAAAACTGTGGAGCCCTACCTGGAGAAGGGTGACATCGTGAGAAGCATGGGCTGCC	1256
Q _y	1556	ATCTTCGTGATCTTATGGCAGCTTAA- - - - CCAATATATGTTCTTGTTCACATCAC	1609
D _b	1257	CTCCGAGATGCCCCGAGCCTGAAGGAGAGCGCTCTCTGTAGTGGTGCCTGACATCGC	1316
Q _y	1610	CACCTCCTTCA CGCTTCTGGTGGGAATCTTCTTTCCCTCTGTTACAGGTATCATGGCTGG	1669
D _b	1317	CACATCCTTACGCGTGTGTGCGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1376
Q _y	1670	ATCAACAGATCTGG 1684	
D _b	1377	GTCAAGCAACTTG 1391	

RESULT 3

835	TGCGAATGTT	835	QY	776	TTTTTTACGCCTTACATGGGTGGGCACAGCTGGAGTTCCTCAGGCTTTTTCGAATGTT
836	TGCGAATGTT	836	QY	836	CCTTATCTGCTGCTGCTCAAAATGTTGACTGTCTATCTCCATGAGTGCCCATGCCACTAA
837	TGCGAATGTT	837	QY	896	TGGAGTGGTGGCAGCTGGGGCTCATACTTTATGATTTCCCGGCACTGGGGCCAGAGTT
838	TGCGAATGTT	838	QY	955	TGGAGTGGTGGCAGCTGGGGCTCATACTTTATGATTTCCCGGCACTGGGGCCAGAGTT
839	TGCGAATGTT	839	QY	957	CGGTGCTGTTTCAGCTGGGGGCTCCTATTTTCATGATCTCTCGTTCACTGGGGGCAGAAAT
840	TGCGAATGTT	840	QY	956	TGGTGGGGCTGTTGGCCTCTGCTTTTATCTTGTTACCACATTTTGCAGACGCCATGTACAT
841	TGCGAATGTT	841	QY	1015	TGGTGGGGCTGTTGGCCTCTGCTTTTATCTTGTTACCACATTTTGCAGACGCCATGTACAT
842	TGCGAATGTT	842	QY	657	TGGAGGTGCTGTGGGGCCTGTGCTTCTACCTGGGAAACAATTTGCAGACGCCATGTACAT
843	TGCGAATGTT	843	QY	1016	CCTTGGTGCATTTGAAATCTTTCTGGTCTATATCGTCCCCCGAGCTGCCATCTTTTCACAG
844	TGCGAATGTT	844	QY	1075	CCTTGGTGCATTTGAAATCTTTCTGGTCTATATCGTCCCCCGAGCTGCCATCTTTTCACAG


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Db 717 CTTGGGGCCATCGAGATCTTGCTGACCTACATGTCCTCCACACAGCTGCCATTTTACCC 776
Qy 1076 TGATGAGCAGCTCAAGGAATCAGCAGCAGTGTAAATAACATGCGTGTCTACGGCACAGC 1135
Db 777 ATCGGTGCTCATGACACGTCGAATGCCACTTTGAACAATATGCGTGTATGGGACCAT 836
Qy 1136 TTTCTTGGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
Db 837 TTTCTTGGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 896
Qy 1196 CTCANTTTTCTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1255
Db 897 CTGCTCTTCTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 956
Qy 1256 GTTCTTCTTCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
Db 957 GTCTATATTTGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1016
Qy 1316 AAGACACATGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1375
Db 1017 GGACGATTTGACATCTGTCGCAAGACAGCTGTAGTGGACAATGAGACAGTGGCCACCCA 1076
Qy 1376 GTTATGGGATTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
Db 1077 GCTATGGAGTTTCTTCTGACAGCCCAACCTTACGACCGACTCTGTGACCCCTACTTT 1136
Qy 1436 TTTTCAACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1495
Db 1137 CATGCTCAACATGTCGACGAGATCCCTGGCATCCCGGGGAGCTGCTGGTGTGCTCCA 1196
Qy 1496 AGAGATCTTTGGAGTATTACTACCCAGGAGAGATCATCGAAAGCCTTACAGCAA 1555
Db 1197 GAAAGAACCTGTGGAGGCTTACTCGAGAGAGGAGTGCATCGTGGAGAGAGATGGGCTGCC 1256
Qy 1556 ATCTTCTGATGCTTTAGGAGCTTAAA-----CATGAATATGTTCTTGTGATCATCAC 1609
Db 1257 CTCGAGATGCTCCGAGCTGAGGAGAGCCTGCTCTGTACGTGGTGTGCTGATCGC 1316
Qy 1610 CACTCTTCTACGCTTCTGTTGGGAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1669
Db 1317 CACATCTTACGCTGCTGCTGGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1376
Qy 1670 ATCAACAGATCTGG 1684
Db 1377 GTCAGAGAACTTG 1391
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RESULT 4

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US-09-146-249A-27
; Sequence 27, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,249A
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..1539, 1859..2383)
; US-09-146-249A-27
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Query Match 12.1%; Score 514.4; DB 3; Length 2384;
Best Local Similarity 66.0%; Pred. No. 3.6e-148;
Matches 762; Conservative 0; Mismatches 387; Indels 6; Gaps 1;

Qy 536 AGGAGATGAATATTTTGTATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACC 595
Db 237 AGGAATTGACTACTATGACAGGAACCTGGCACTGTTTGGAGGAGAGCTGGACATCGGCC 296
Qy 596 GAAAGTGTCTTCCCTCTCAACCGCATGGCCAAATTTACACTAATCTGACTCAAGAGAGAAA 655
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Qy 656 GGACATGAAGAGCAGCAGAAACATCACTGAAGGAGGAAAGAGCCCAACAGACCCCA 715
Db 357 AGAGCATGAGGAGGCGGAGAGTGGGGAGGCGACCGCGGAGGCGAGCGGACCCAG 416
Qy 716 AATGGGTACCTTTCATGGGTGTCTACCTCCCATGTCTACAAATATTTTGGAGTGTCT 775
Db 417 CATGGCACCTCATGGGGTGTACCTGCTGCTGCGAGATATCTTTGGGTTATCT 476
Qy 776 TTTTATACGCTTACATGGGTGTGGGACAGCTGGAGTCTTCAGGCTTTTGCATTTGT 835
Db 477 CTTCTCGGCTGACCTGGATGTTGGGACAGCAGGAGTGTCTACAGGCTCTCTCATCT 536
Qy 836 CTTTATCTGCTGCTGTACAAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAA 895
Db 537 GCTTATCTGCTGTGTGTACCTGCTGACGGCCATCTCCATGAGTGCCATTCGCCACCA 596
Qy 896 TGGAGTGTGCGAGCTGGGGCTCATCTTTATGATTTTCCGGGACCTGGGCCACAGT 955
Db 597 CGGTGTGTTCCAGCTGGGGCTCTCTTTATGATCTCTGTTACCTGGGGCCAGAT 656
Qy 956 TGGTGGGCTGTGGCTCTGCTTTATCTTTGGTACCAATTTGACAGCAGCATGTACAT 1015
Db 657 TGGAGTGTGTTGGGCTGTGCTTCTACCTGGGAAACAACTTCGACAGCAGCATGTACAT 716
Qy 1016 CTTTGGTGCATTTGAAATCTTTCTGGTCTATATCTGCTCCCGAGCTGCCATCTTTCACAG 1075
Db 717 CTTGGGGCCATCGAGATCTTGTGACTACATTTGCCCTACATTTGCCCTCTCTTTTACCC 776
Qy 1076 TGATGAGCAGCTCAAGGAATTCAGCAGCAGTCTAAATAACATGCTGTCTACGACAGC 1135
Db 777 ATCGGTGCTCATGACAGCTGGAATGCCACTTTTGAACAATATGCTGTGTATGGACCAT 836
Qy 1136 TTTCTTGGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
Db 837 TTTCTTGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 896
Qy 1196 CTCANTTTTCTGGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1255
```

Db 897 CTCGCTTTCTCGGCTGTGTGATCATCTCCATCTCTCCATCTATGCTGGGGCATAAA 956
QY 1256 GTCTTCTTTTGTCTCCACACTTCCCGTCTGCACTGCTGGTAAACCGACACTTTTCATC 1315
Db 957 GTCTATATTTGACCTTCCCGTGTTCGGTATGCACTGCTGGCAACAGGACCTCTCCGG 1016
QY 1316 AAGACACATTTGAGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAA 1375
Db 1017 GGACCAAGTTTGACATCTGTGCAAGACAGCTGTAGTGGACAATGAGACAGTGGCCACCA 1076
QY 1376 GTATGGGATTTCTTGTAACTCGAGTCAATTTTCAATGCGCACTGTGATGAATACTT 1435
Db 1077 GCTATGGAGTTTCTTCTGCCACAGCCCAACCTTACGACCGACTCTGTGACCCCTACTT 1136
QY 1436 TGTCAACAATAGCTTCAATCCAGGCAATCTCGATTTGGTGTAGTGTATTAATTAC 1495
Db 1137 CATGCTCAACATGTGACCGAGATCTCTGGCATCCCGGGGAGCTGTGGTGTGCTCA 1196
QY 1496 AGAATCTTTTGGAGTAATTACCTACCAAGGAGAGATCATCGAAAGCCTTCAGCCAA 1555
Db 1197 GGAAACCTGTGGAGCGCTACTTGGAGAGGAGTGCATCTGTGGAGACATGGGCTGCC 1256
QY 1556 ATCTTCTGATGCTTAGGAGCTTAAA-----CAGTAATATGTTCTTTGTGACATCAC 1609
Db 1257 CTCGCGAGATGCCCCGAGCCTGAAGGAGAGCCTGCTCTGTAGTGTGCTGACATCGC 1316
QY 1610 CACTCTCTTCACTTCTGCTGGGATCTTCTTCCCTCTGTTACAGGTATCATGCTGG 1669
Db 1317 CACATCTTACCGTCTGTGCGCATCTTCTTCCCTCTGTAACAGAGTATGGCATGT 1376
QY 1670 ATCAACAGATCTGG 1684
Db 1377 GTCAGCAGGAATTG 1391

RESULT 5

US-08-206-188B-27
; Sequence 27, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wiegler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..1539, 1859..2383)
US-08-206-188B-27

Query Match 12.1%; Score 514.4; DB 3; Length 2384;
Best Local Similarity 66.0%; Pred. No. 3.6e-148;
Matches 762; Conservative 0; Mismatches 387; Indels 6; Gaps 1;

QY 536 AGGAGATGAATATTTTGTATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACC 595
Db 237 AGGAATTGACTATATGACAGGAACCTGGCACTGTTTGGAGGAAGAGCTGGACATCCGCC 296
QY 596 GAAGGTGTCTTCCCTCTCAACCGCATGGCCAAATTACATAATCTGACTCAAGGAGCAAA 655
Db 297 AAAGTATCTGCTCTTCTGGGAAAGCTCGTCAGCTACACCAACCTCACCCAGGGGCCAA 356
QY 656 GGAACATGAAGAGGAGAGAAACATCATGAAGGGAAGAAAGAGCCACCAAGACCCCA 715
Db 357 AGAGCATGAGGAGGCGGAGAGTGGGGAGGGCAACCCGCGGAGGCGAGCCGAGGCCAC 416
QY 716 AATGGTACCTTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGTACT 775
Db 417 CATGGCAACCTCATGGGGTGTACTGCTGCTGCTGCGAGAAATATCTTTGGGGTATCT 476
QY 776 TTTTTCACGCTTACATGGGTGTGGGCACAGCTGGAGTCTTTCAGGCTTTTGCATTTGT 835
Db 477 CTCTCTGGGCTGACCTGGATGGTGGGCACAGCAGGTGTGTACAGGCCCTCTCATCT 536
QY 836 CTTATCTGCTGCTGTACAAATGTTGACTGTCTATCTCCATGAGTGCATTTGCCACTAA 895
Db 537 GCTTATCTGCTGTGTGTACCTCTGACGGCCATCTCCATGAGTGCATTCGCCACCAA 596
QY 896 TGGAGTGTGCGAGCTGGGGCTCATCTTATGATTTCCCGGACACTGGGCCCAAGATT 955
Db 597 CGGTGTGTTCCAGCTGGGGCTCTTATTCATGATCTCTGTTCACTTGGGGCAGAAAT 656
QY 956 TGGTGGGCTGTGGCCCTCTCTTTTATCTTGTGTAACCAATTTGAGCAGGCAATGATCAT 1015
Db 657 TGGAGTGTCTGTGGCCCTGTCTTCTACCTGGGAACAACATTTGCGCAGCAGCATGTACAT 716
QY 1016 CTTGTGTCCTAATGAATCTTCTGGTCTATATCGTCCCGCAGCTGCATCTTTTCACAG 1075
Db 717 CTTGGGGCCATCGAGATCTTGTGACTACATTTGCCCCACAGCTGCCATTTTTCACC 776
QY 1076 TGATGACGCACTCAAGGAATCAGAGCCATGCTAAATAACATGCTGTCTAGGGCAGCAGC 1135
Db 777 ATCGGCTGTCTATGACACGTCGAATGCCCATTTTGAACAATATGCTGTGTATGGACCAT 836
QY 1136 TTTCTTGTCTCTATGATGATTTAGTGTATTTATCGGCTAGCTATGTGAACAAGTTTGC 1195
Db 837 TTTCTGTGCTTATGACCCCTGGTGTGTGTGGGGTCAAGTATGTGAACAATTTGC 896
QY 1196 CTCANTTTTCTGGCCTGTGTCTATTTGTCTCATCTTGGCCATCTATGCTGGAGCCATCA 1255
Db 897 CTCGCTCTTCTGGCCTGTGTGATCATCTCCATCTCTCCATCTATGCTGGGGCATAAA 956
QY 1256 GTCTTCTTTTGTCTCTCCACACTTCCCGTCTGCACTGCTGGTAAACCGCACTCTTTTCATC 1315
Db 957 GTCTATATTTGACCTCTCCGTTTTCGGTATGCAATGCTGGCAACAGGACCTGTCCCG 1016
QY 1316 AAGACACATTTGACGTTTGTCTTAAGACCAAGGAAATTAACAACATGACAGTCCCATCAA 1375
Db 1017 GGACCAAGTTTGACATCTGTGCAAGACAGCTGTAGTGGACAATGAGACAGTGGCCACCA 1076
QY 1376 GTTATGGGATTTCTTGTAACTCGAGTCAATTTTCAATGCCACTGTGATGAATACTT 1435
Db 1077 GCTATGGAGTTTCTTCTGCCACAGCCCAACCTTACGACCGACTCTGTGACCCCTACTT 1136

QY 1436 TGTTTCAATACGTCACCTTCAATCCAGGGGCAATTCCTGGAATGGCTAGTGGTATTAATTAC 1495
DB 1137 CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGCTGTGTGCTCCA 1196
QY 1496 AGAGAATCTTTGGAGTAAATTAACCTACCCAGGAGAGATCATCGAAAGCCTTCAGCCAA 1555
DB 1197 GGAAACCTGTGGAGCGCTACTCGAGNAGGCTGACATCGTGGAGAGCATGGGCTGCC 1256
QY 1556 ATCTTCTGATGCTTAGGAGCTTAAA-----CCATGAATATGTTTGTGACATCAC 1609
DB 1257 CTCGAGATGCCCCGAGCCTGAAGAGAGCCTGCTCTGTACGTGGTCTGACATCGC 1316
QY 1610 CACCTCCTTACGCTTCTGTTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGGCTGG 1669
DB 1317 CACATCCTTCAACCGTGTGTCGGCATCTTCTTCCCTTCTGTAACAGGTATGGCGATGCT 1376
QY 1670 ATCAAAACAGATCTGG 1684
DB 1377 GTCAGCAGGAACCTTG 1391

RESULT 6

PCT-US91-02714-25

; Sequence 25, Application PC/TUS9102714

; GENERAL INFORMATION:

; APPLICANT: Wigler, Michael H.

; APPLICANT: Colicelli, John J.

; TITLE OF INVENTION: Cloning by Complementation and Related

; TITLE OF INVENTION: Processes

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESS: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/02714

; FILING DATE: 19910419

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/511,715

; FILING DATE: 20-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25447

; REFERENCE/DOCKET NUMBER: 27805/30197

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELETYPE: 25-3856

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2384 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1541

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1859..2383

PCT-US91-02714-25

Query Match 12.1%; Score 514.4; DB 5; Length 2384;

Best Local Similarity 66.0%; Pred. No. 3.6e-146;

Matches 762; Conservative 0; Mismatches 387; Indels 6; Gaps 1;

QY 536 AGGAGATCAATATTTTGATAAATAATTTGGCACTCTTTCAGGAGAAATGGACACCAGACC 595
DB 237 AGGAATTGACTACTATGACAGAAACCTGGCACTGTTTGGAGAGAGCTGGACATCCGCC 296
QY 596 GAAGGTGCTTCCCTCCCTCAACCGCATGGCCAAATTACACTAATCTGACTCAAGGAGCAAA 655
DB 297 AAAGGTATGCTCTCTTCTGGGAAAGCTCTGAGCTACACCACTCACCAGGGGCCAA 356
QY 656 GGAACATGAAGAGCAGAAAAATCATCACTGAAGGAAAAAGAGCCCAACCAAGACCCCCA 715
DB 357 AGAGCATGAGGAGCGGAGAGTGGGGAGGCGACCGCGGAGGGGAGCCGAGGACCCAG 416
QY 716 AATGGGTACCTTTCATGGGTGCTACCTCCCATGCTACAAAATATTTTGGAGTGATCCT 775
DB 417 CATGGGCACCTCATGGGGGTGTACCTGCCCTGCTGCAGAAATATCTTTGGGGTTATCCT 476
QY 776 TTTTTCACGCTTACATGGGTGGGCGACAGCTGGAGTCTTTCAGGCTTTTGGCAATTGT 835
DB 477 CTTCCTGGGCTGACCTGGATGGGCGACAGAGGTGTGTACAGGCCCTCCTCATGCT 536
QY 836 CCTTATCTGCTGCTGTACAAATGTTGACTGCTACTCTCCATGAGTGCCATTGGCCACTAA 895
DB 537 GCTTATCTGCTGCTGTGTACCTGCTGAGCGCCATCTCCATGAGTGCCATGCGCCACCA 596
QY 896 TGGAGTGTGCGAGCTGGGGCTCATCTTATGATTTCCCGGGGACCTGGGGCCAGAGTT 955
DB 597 CGGTGTGGTTCAGCTGGGGCTCCTATTTTATGATCTCTGCTTCACTGGGGCCAGAA 656
QY 956 TGGTGGGCTGCTGGCCCTCTCTTTATCTTGGTACCACTTTGCGAGAGCCATGATACAT 1015
DB 657 TGGAGTGTGCTGGGGCTGTGCTTCTACCTGGGAAACAACATTCGAGAGCCATGATACAT 716
QY 1016 CCTTGGTGCCATGAAATCTTTCTGGTCTATATCTGCCCGGAGCTGCCATCTTTACAG 1075
DB 717 CCTGGGGCCATCGAGATCTTGTGCTGACCTACATATGCCCCACCGCTGCCATTTTACCC 776
QY 1076 TGATGAGCACTCAAGGAATCAGCAGCATGCTTAAATAACATGCTGTCTAGGGCAGC 1135
DB 777 ATCGGGTCTCATGACAGCTCGAATGCGACCTTTTGAACAATATGCTGTGTATGGACCAT 836
QY 1136 TTTCTGTGCTCTTATGTTAGTGTATTTATCGGGTACGCTATGTAACAAGTTTGC 1195
DB 837 TTTCTGGCTTCAAGACCTTGGTGGTGTGTTGGGGGTCAAGTATGTGAACAATTTGC 896
QY 1196 CTCANTTTTCTGGCCTGTGTCTATTTGTCTCATCTTGGCCATCTATGCTGGAGCCATCAA 1255
DB 897 CTCGCTCTTCTGGCTGTGTGATCACTCCATCTCTCCATCTATGCTGGGGCATAAA 956
QY 1256 GTCTTCTTTTGTCTCTCCACACTTTCGCGGTCTGATGCTGGGTAAACCGCATCTTTTCATC 1315
DB 957 GTCTATATTTGACCTCTCCGCTGTTTCCGGTATGATGCTGGGCAACAGGACCTGTCCCG 1016
QY 1316 AAGACACATTTGACCTTGTCTTAAGCAAGGAATTAACAACATGACAGTCCCATCAA 1375
DB 1017 GGACCACTTTGACATCTGTGCAAGACAGCTGTATGTGACAAATGAGACAGTGGCCACCA 1076
QY 1376 GTTATGGGATTTCTTGTAACTCGAGTCAATTTTTTCAATGCCACCTCTGTGATGAATCTT 1435
DB 1077 GCTATGGAGTTTCTTCTGCCACAGCCCAACCTTACGACCGACTCTCTGTGACCCCTACTT 1136
QY 1436 TGTTCAAAATACCTCACTTCAATCCAGGGCATTTCTGGATTGGCTAGTGTATTAATTAC 1495
DB 1137 CATGCTCAACAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGTGCTGTGCTCCA 1196
QY 1496 AGAANAATTTTGGAGTAAATTAACCTACCCAGGAGAGATCATCGAAAGCCCTTCAGCCA 1555
DB 1197 GGAAAACTGTGGAGCGCCTACCTGGAGAGGGGTGACATCTGTGGAGAGCATGGGCTGCC 1256

QY 1556 ATCTTCTGATGCTTAGGAGCTTAA-----CCATGAATATGTTCTTTGTCATCAC 1609
Db 1257 CTCGGAGATGCCGAGCCTGAAGAGAGCCTGCTCTGACGTGGTCGCTGACATGC 1316
QY 1610 CACCTCTTACGCTTCTGGTGGGAATCTTCTCCCTCTGTACAGGTATCATGGCTGG 1669
Db 1317 CACATCTTACCGTGCTGGTCGGCATCTTCTTCCCTTCTGTAAACAGGTATGGCGATGGT 1376
QY 1670 ATCAACAGATCTGG 1684
Db 1377 GTCAGCAGGAAGTTG 1391

RESULT 7

US-09-016-434-294
; Sequence 294, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 294:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LIVRUT01
; CLONE: 1755202
US-09-016-434-294

Query Match 5.3%; Score 226; DB 4; Length 227;
Best Local Similarity 99.6%; Pred. No. 1.1e-59;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2864 CAGCAATGTGAGCAATTTTCTGAGGCAACATTGATGTGTGGATTGTGATGATGG 2923
Db 1 CAGCAATGTGAGCAATTTTCTGAGGCAACATTGATGTGTGGATTGTGATGANGG 60
QY 2924 GGGGATGCTTATGCTACTACCATCTTCTGAAACAGCAACAGGTGTGGCGAAGTGCAG 2983
Db 61 GGGGATGCTTATGCTACTACCATCTTCTGAAACAGCAACAGGTGTGGCGAAGTGCAG 120

QY 2984 CATACGATCTTACAGTAGCCCAATTAGAAGACAACAGATATCCAAATGAAGAGGACCT 3043
Db 121 CATACGATCTTACAGTAGCCCAATTAGAAGACAACAGATATCCAAATGAAGAGGACCT 180
QY 3044 AGCCACCTTCTATATACCTTACCCATTTAGAGCGGAGGTAGAGTGG 3090
Db 181 AGCCACCTTCTATATACCTTACCCATTTAGAGCGGAGGTAGAGTGG 227

RESULT 8

US-09-016-434-464
; Sequence 464, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 464:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSN0T16
; CLONE: 2233388
US-09-016-434-464

Query Match 3.2%; Score 136.4; DB 4; Length 254;
Best Local Similarity 74.6%; Pred. No. 6.1e-32;
Matches 170; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 3390 CCGGACCACTCCAAATGTGAGCGGATGCATACAGCAGTGAAACTCAACGAGGTATAGTT 3449
Db 5 CCGGACCACTCCAAATGTGAGCGGATGCACACGGTGTGAAGCTCAATGGCGTCGCTC 64
QY 3450 AACAAAGTCCCATGAAGCAAGCTGGTTTATTGAATATGCCAGGCCACCCGAAACCT 3509
Db 65 AACAAAGTCCCATGAAGCTGGTTTATTGAATATGCCAGGCCACCCGAAACCT 124
QY 3510 GAGGAGTGAAGAACTACATGAGTTCCTAGAGGTCTCTACCGAGGACTAGAGCGAGTC 3569
Db 125 CAGGAGAGCGAGAACTACATGAGTTCCTAGAGGTCTCTACCGAGGACTAGAGCGAGTC 184

[illegible]

RESULT 9
US-09-016-434-614
; Sequence 614, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 614:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2508812
US-09-016-434-614

Query Match	2.9%	Score 123.4;	DB 4;	Length 235;
Best Local Similarity	72.4%;	Pred. No. 6.1e-28;		
Matches 160;	Conservative 0;	Mismatches 61;	Indels 0;	Gaps 0;
QY	3012	GAAGACAACAGTATCCAAATGAAGAGGAGCTAGCCACCTTCCTATATCATCTACTTACGCATT	3071	
DB	2	GACGACACAGCATCCAGATGAGAGGAGCTGCAGATGTTCTGTATCATCTTGGCGATC	61	
QY	3072	GAGCGGAGGTAGAAGTGTGGAGATGCATGACAGTGATATATCAGCATATATCTTACGAG	3131	
DB	62	AGCGCCGAGGTGGAGGTGTGGAGATGGTTGAAACGACATATCTGTTTCACTACGAG	121	
QY	3132	CGCACATTGATGATGAACAAAGTCCAGATCTTCGGCACATCGGCTTATCCAAACA	3191	
DB	122	AGGACACTATGATGAGCAGAGTCCAGATCTGAGCAGATGACGCTGTCCAAGAC	181	
QY	3192	GAGCGAGACAGAGGCACAATTTGGTGAAGACCGAAACTC	3232	
DB	182	GAGCAGGAGCGAGGCCGAGCTGATCCAGCAGGAACAC	222	

RESULT 10
US-09-016-434-475
; Sequence 475, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 475:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVARTUT01
; CLONE: 2254533
US-09-016-434-475

Query Match	2.7%	Score 116;	DB 4;	Length 231;
Best Local Similarity	68.4%;	Pred. No. 1.2e-25;		
Matches 158;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;
Qy	2341	GGGGTGATGATACCGCTGGGCTGTCCCTCAGTGCAGCCCGGTTTGTCTTTCGATTGG	2400	
Db	1	GGGGCGATGGCATCCGTGGCCCTATCCCTGACGCCCGCCGCTACGCCCTGCTCGGCGTGG	60	
Qy	2401	AGGAAGGACCTCCACACACTAAAAACTGAGGCGCTCAGTTGTGTATTACTGAAACTAG	2460	
Db	61	AGCACGGTCCCCCCACACAAAGAACTGGAGGCGCCAGGTGGTGGTGATGCTGAACTGG	120	
Qy	2461	ATGAAGACTTTACATGTCGAAGCATCCTCGGCTCCTCACTTTGCCTCACAAGCTCAAAAGCAG	2520	
Db	121	ACGCGGAACAGGCCGTGAAGACCCCGGCTGCTTCCTTCAGNCGCACTGAAGCCCG	180	
Qy	2521	GAAGAAGTNTACTATTGTGGGCTCTGTTCATCGTGGGGAACCTTCCTAGAGA	2571	
Db	181	GCAAAGGCTTGACCATCTGGCTGGGCTCGGTGGTGGANGGACCGTACTGGACA	231	

RESULT 11
US-09-016-434-371


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; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match 1.4%; Score 60.6; DB 1; Length 7218;
Best Local Similarity 4.6%; Pred. No. 2.2e-07;
Matches 18; Conservative 223; Mismatches 152; Indels 0; Gaps 0;

QY 2986 TAGCGATCTTACAGTAGCCCAATAGAGACACAGTATCCAAATGAGAGAGGACCTAG 3045
DB 1437 TACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1378

QY 3046 CCACCTTCTATATCATCTAGCCATTGAGCGGAGGTAGAGTGTGGAGATGCATGACA 3105
DB 1377 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1318

QY 3106 GTGATATATCAGCATATATCTACGAGCGCAGCTTTGATGATGGAACAAAGGTCACAGATGC 3165
DB 1317 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1258

QY 3166 TTCGCACATCGCGGTATCCAAACAGAGCAGAGACAGAGCACAATGTGGAAGACC 3225
DB 1257 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198

QY 3226 GAACTCAATGCTACGATTGACACAGCTTGGCTCTGATGAGACCAAGACAGACAGAACT 3285
DB 1197 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1138

QY 3286 ATCAGGAGAAGGTGCATGACTTTGGACAAAGACAGTACATGATGCCATCCCGGACACAA 3345
DB 1137 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1078

QY 3346 AAGCAAGTCAATGAAGATTCCAGGACCTGC 3378
DB 1077 RRRRRRRRRRATCGAAGCTCCCTCGACCTGC 1045
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RESULT 14
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match 1.2%; Score 51.8; DB 1; Length 7218;
Best Local Similarity 4.2%; Pred. No. 0.00012;
Matches 17; Conservative 222; Mismatches 165; Indels 0; Gaps 0;

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DB 1038 CTGGCTGAGGTGAGGGAGCTTGCATTTTTTTTTTTTTTTTTTTTTTTTTT 1097

QY 1002 GCAGCCATGTACATCTTGTGTGCATTAATCTTTCTGTCTATATCGTCCCGAGCT 1061
DB 1098 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1157

QY 1062 GCATCTTTACAGTATGAGCAGCTCAAGAAATCAGCAGCATGCTAAATACATGCT 1121
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QY 1122 GTCTACGCGCAGCTTCTTGTGCTCTTATGATGATGATGATGATGATGATGAT 1181
DB 1218 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1277

QY 1182 GTGAACCAAGTTGCTCANTTTCTGCGCTGTGCTATTGTGCTCATCTTGGCCATCTAT 1241
DB 1278 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1337

QY 1242 GCTGGAGCCATCAAGTCTTCTTTGCTCTCCACACTTCCGGTCTGCATGCTGGTAAC 1301
DB 1338 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1397

QY 1302 CGCACTCTTTCATCAACACACATGAGCTTGTGCTCTAAGACCA 1345
DB 1398 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCA 1441
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RESULT 15
US-09-599-360B-64
; Sequence 64, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
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; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 64
; LENGTH: 1355
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1152
; NAME/KEY: sig_peptide
; LOCATION: 238..339
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: seq SIFLLSFPDSNG/KA
; NAME/KEY: polyA_signal
; LOCATION: 1298..1303
; NAME/KEY: polyA_site
; LOCATION: 1324..1355
US-09-599-360B-64

Query Match      1.0%; Score 43.2; DB 4; Length 1355;
Best Local Similarity 50.0%; Pred. NO. 0.015;
Matches 108; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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Db 1140 CATCTGAAACTTGAAGAAATCTGGAGAAATTTCTGAAGATGTAAACCAGATCTTTCCAAA 1199

QY 4104 ATGCAAAACATTTTATAGCTATATTTCTTTAGTATATACCCACTGCTGTAATTTTATATTAGG 4163
Db 1200 TACAAAGATTAGATAAATTTGTTCTTATTGTACTTTATGTAGAGAGAAATTTTCAGCTTCTC 1259

QY 4164 ATACTTAACCTTGAACATGCTGCGCCTCTACTTCTTCAAAAACATCCCCCAAATACC 4223
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QY 4224 AGATTTAAATATCCRAAAAAAATAAAAAA 4259
Db 1320 AGCTAAAAAATAAAAAAATAAAAAA 1355
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Search completed: November 27, 2003, 00:40:53
Job time : 232 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: November 26, 2003, 16:49:40 ; Search time 15085 Seconds
(without alignments)
11552.868 Million cell updates/sec
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
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- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
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- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	4241.4	99.6	4260	9	AF105366	AF105366 Homo sapi
2	3995.2	93.8	4453	9	AF477977	AF477977 Homo sapi
3	3657.8	85.9	3674	9	HSM801017	AL117500 Homo sapi
4	3584.4	84.1	3767	9	AF108831	AF108831 Homo sapi
5	3445.2	80.9	3453	9	AF116242	AF116242 Homo sapi
6	2960.8	69.5	6120	10	AF211854	AF211854 Mus muscu
7	2735.2	64.2	5964	10	AF211855	AF211855 Mus muscu
8	1674	39.3	3726	6	AX401991	AX401991 Sequence
9	1674	39.3	3726	10	RNU5815	U55815 Rattus norv
10	1660.4	39.0	3734	4	OCKCC	U55053 Oryctolagus
11	1652.6	38.8	3764	10	AF121118	AF121118 Mus muscu
12	1652.6	38.8	3775	10	AF047339	AF047339 Mus muscu
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17	1639.4	38.5	3351	4	AF028807	AF028807 Sus scro
18	1632.2	38.3	3307	4	AF515770	AF515770 Ovis arie
19	1584	37.2	3768	9	AF054506	AF054506 Homo sapi
20	1509.4	35.4	3761	9	AF054505	AF054505 Homo sapi
21	1419.4	33.3	5239	9	AF105365	AF105365 Homo sapi
22	1416.2	33.2	5155	10	AF087436	AF087436 Mus muscu
23	1395.4	32.8	3305	9	AB033002	AB033002 Homo sapi
24	1395.4	32.8	5907	9	AF208159	AF208159 Homo sapi
25	1385.2	32.5	3655	10	AF332063	AF332063 Mus muscu
26	1385.2	32.5	3656	10	AF332064	AF332064 Mus muscu
27	1385.2	32.5	5735	10	AK122460	AK122460 Mus muscu
28	1377.8	32.3	5566	10	RNU5816	U55816 Rattus norv
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31	1074.6	25.2	4318	9	AK024493	AK024493 Homo sapi
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33	1012	23.8	4143	9	AK024497	AK024497 Homo sapi
34	845	19.8	3597	3	AY118761	AY118761 Drosophi
35	729.2	17.1	2635	3	AF116120	AF116120 Ciona int
36	711	16.7	783	9	F314931826	AF314931 Homo sapi
37	703.4	16.5	124343	2	AC079188	AC079188 Homo sapi
38	703.4	16.5	197568	9	AC079203	AC079203 Homo sapi
39	677.8	15.9	2518	9	AK097808	AK097808 Homo sapi
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41	514.4	12.1	2384	6	AR083652	AR083652 Sequence
42	514.4	12.1	2384	6	I22489	I22489 Sequence 27
43	466.8	11.0	4478	10	BC051061	BC051061 Mus muscu
44	434	10.2	489	9	F314931S01	AF314931 Homo sapi
45	434	10.2	95800	9	AC021822	AC021822 Homo sapi

ALIGNMENTS

RESULT 1
AF105366
LOCUS AF105366 4260 bp mRNA linear PRI 20-JUN-1999
DEFINITION Homo sapiens K-Cl cotransporter KCC3a mRNA, alternatively spliced,
complete cds.
ACCESSION AF105366
VERSION AF105366.1 GI:5106522
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4260)
AUTHORS Mount,D.B., Mercado,A., Song,L., Xu,J., George,A.L. Jr., Delpire,E.
and Gamba,G.

TITLE Cloning and characterization of KCC3 and KCC4, new members of the cation-chloride cotransporter gene family
J. Biol. Chem. 274 (23), 16355-16362 (1999)
MEDLINE 99278405
PUBMED 10347194

REFERENCE 2 (bases 1 to 4260)

AUTHORS Mount, D.B.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1998) Division of Nephrology, Department of Medicine, Vanderbilt University Medical Center, S-3223 Medical Center North, Nashville, TN 37232-2372, USA

FEATURES Location/Qualifiers

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/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="15"

/map="15q14"

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/codon_start=1

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/protein_id="AAD39742.1"

/db_xref="GI:5106523"

/translation="MHPPETTTKMASVRPMVPTTKIDIPGLSDTSPDLSSRSSRVR
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QGAKEHEAEANTTEGKKPKTPQMGTFMGVYLPCLONIFGVILFLRLTVVGTAGVL
QAFVILICCCCTMLTAISMSALATNGVVPAGGSYFMLSALGPEFGAGVLCFYLT
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LTAABGLILLASDLVAPILSMFFLMCLFLVNLACALQTLRLTPNRPRTYTHWA
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TIYS"

BASE COUNT 1165 a 977 c 972 g 1146 t

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Query Match 99.6%; Score 4241.4; DB 9; Length 4260;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4254; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

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DB 301 GTCCTCCGGAAAGCGTCTGTAACCAAGCGGAGTGAGGCTATGAGTGAGATGTCTGGGG 360
QY 361 CCACACCTTCGCTGGCAACTGTGTGACCTGGATCCACCCAGTGACCCGAGCTTCTTCACCCCC 420
DB 361 CCACACCTTCGCTGGCAACTGTGTGACCTGGATCCACCCAGTGACCCGAGCTTCTTCACCCCC 420
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DB 421 AGGATGTTCATCGAGGACCTGAGTCAAGAACTCCATCACAAGGGGAAACACAGCCAACTGTTAG 480
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QY 541 ATGAATATTTTGTATAAAAAATTTGGCACTCTTTGAGGAAAGAAATGACACACGACCGAAGG 600
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DB 601 TGTCTTCCTCCTCAACCCGATGGCCAAATTAACATTAATCTGACTCAAGGAGCAAAAGGAAC 660
QY 661 ATGAAGAGCGAGAAAACATCACTGAGGAAAAGAACCCCAAGACCCCGCCAAATGG 720
DB 661 ATGAAGAGCGAGAAAACATCACTGAGGAAAAGAACCCCAAGACCCCGCCAAATGG 720
QY 721 GTACCTTCATGGGTGCTCACTCCATCTCCATCTACAAAATATTTTGGAGTGATCCTTTTTT 780
DB 721 GTACCTTCATGGGTGCTCACTCCATCTCCATCTACAAAATATTTTGGAGTGATCCTTTTTT 780
QY 781 TACGCTTTACATGGGTGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGCATTTGTCCTTA 840
DB 781 TACGCTTTACATGGGTGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGCATTTGTCCTTA 840
QY 841 TCTGCTGCTGCTGTAACAATTTGACTGCTATCTCAGTGGCCATTTGCCACTAATGGAG 900
DB 841 TCTGCTGCTGCTGTAACAATTTGACTGCTATCTCAGTGGCCATTTGCCACTAATGGAG 900
QY 901 TGGTCCAGCTGGGGGCTCATACTTTATGATTTCCCGGCGACTGGGCGCCAGAGTTTGGTG 960
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1681 CTGGAGATCTGAAAGATGCTCAGAAATCTATTCGATGGTACTATCCTTGGCATCCTGA 1740
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1741 CCACCTCCTTGTATTAAGCAATGTTGCTCTTTTGGTGCAATGATTGAAGGGGTG 1800
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1801 TTCTCAGAGACAAAGTTCGGTGAATGCTGTGAAGGTAAATTTGGTGAAGCACTTATCTT 1860
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1861 GGCCATCCCATGGTGATGTTATGCTCTCTCTTTCAACATGTCGGGCTGACATTC 1920
1861 GGCCATCCCATGGTGATGTTATGCTCTCTCTTTCAACATGTCGGGCTGACATTC 1920
1921 AGAGCTCACAGGTGACCGAGGTGCTACAAGCTATTGCCAAGGATAACATCATAACCGT 1980
1921 AGAGCTCACAGGTGACCGAGGTGCTACAAGCTATTGCCAAGGATAACATCATAACCGT 1980
1981 TTCTGAGGGTTTTGGCCACAGCAAGCAATGGGGAACCTACCTGGGCTTTACTTTAA 2040
1981 TTCTGAGGGTTTTGGCCACAGCAAGCAATGGGGAACCTACCTGGGCTTTACTTTAA 2040
2041 CTGCTGCCATTTGCAGAGCTTGGAACTACTTGTGCTCTCTGATCTTGTGGCCCAATTC 2100
2041 CTGCTGCCATTTGCAGAGCTTGGAACTACTTGTGCTCTCTGATCTTGTGGCCCAATTC 2100
2101 TTTCCATGTTTTTCTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGCAACAT 2160
2101 TTTCCATGTTTTTCTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGCAACAT 2160
2161 TACTTCGAACACCCAACTGGAGACCCCGATTCCTACTAGCAATTTGGGCCCTTTCTTCA 2220
2161 TACTTCGAACACCCAACTGGAGACCCCGATTCCTACTAGCAATTTGGGCCCTTTCTTCA 2220
2221 TGGGAATCAGTATCTGCTGGCTCTGATGTTCAATTTCTTCTGCTGATTTATGCCATTGTAG 2280
2221 TGGGAATCAGTATCTGCTGGCTCTGATGTTCAATTTCTTCTGCTGATTTATGCCATTGTAG 2280
2281 CCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGGAGCTGAGAAAGAT 2340
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2341 GGGGTGATGTTATCGTGGGCTGCTCCTCAGTGAGCCCGGTTTGTCTTGTCTTGTGATGG 2400
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2401 AGGAAGGACCTCCACACATAAAGCTGAGGCTCAGTTCCTGTTATTAAGTAACTAG 2460
2401 AGGAAGGACCTCCACACATAAAGCTGAGGCTCAGTTCCTGTTATTAAGTAACTAG 2460
2461 ATGAAGACTTACATGTCAGAGCATCCTCGCCTCCTCACCTTTGCTTCAAGAGCAG 2520
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2521 GAAAGGTTNTCATTATTTGGGCTCTGTCTCATCGTGGGAACTTCTTAGAGAACTACGGTG 2580
2521 GAAAGGTTNTCATTATTTGGGCTCTGTCTCATCGTGGGAACTTCTTAGAGAACTACGGTG 2580
2581 AAGCTTTAGCTGCTGAGCAGACCAATAAGACACCTTAATGGAGGACAGAAAGGTAAAGGAT 2640
2581 AAGCTTTAGCTGCTGAGCAGACCAATAAGACACCTTAATGGAGGACAGAAAGGTAAAGGAT 2640
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2641 TCTGCCAGCTGGTGGTGGCCGCAAGCTGAGAGAGGCAATTTCCACCTCATCCAGTCAAT 2700
2701 GTGGCCTTGGGGGATGAGCAGACCAACACGCTGGTGGTGGGCTGAGTGGTGGGCTG 2760
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2941 TACCATTCTCTACTCAAAACAGCACAAGGTGTGGCAGAAAGTGCAGATACCGATCTTCACAG 3000
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3121 ATACTTACGAGCGACATTTGATGATGAAACAAAGTCCCAGATCTTCGGCACAATGGGC 3180
3121 ATACTTACGAGCGACATTTGATGATGAAACAAAGTCCCAGATCTTCGGCACAATGGGC 3180
3181 TATCCAAAACAGAGCGAGACAGAGGACCAATTTGGTGAAGACCCGAACTCAATGCTTAC 3240
3181 TATCCAAAACAGAGCGAGACAGAGGACCAATTTGGTGAAGACCCGAACTCAATGCTTAC 3240
3241 GATTGACAGGATTTGGCTCTGATGAGGACGAGACAGAAACCTTATCAGGAGAGGTGC 3300
3241 GATTGACAGGATTTGGCTCTGATGAGGACGAGACAGAAACCTTATCAGGAGAGGTGC 3300
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3361 AAGGATTTCCAGGACCTCTTAAACATGCGCTCCGACCACTCAATGTGAGGCGGATGCATA 3420
3421 CAGCAGTGAACCTCAACAGAGTTATAGTTAAACAGTCCCATGAAGCAAGCTGTTTAT 3480
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3601 TCACCATTTATTATCAATACCTACTCTCTGAATGACCGTCTTGACCTGTTTCTTAAAGGCC 3660

Db 1097 TGCCAGCTGGGGCTCATACTTTATGATTTCCGGGCACTGGGCCAGAGTTTGTGGGG 1156
Qy 964 CTGTGGCCCTCTGCTTTTATCTTGTAACACATTTGACAGACCCAGTACATCTTGTGG 1023
Db 1157 CTGTGGCCCTCTGCTTTTATCTTGTAACACATTTGACAGACCCAGTACATCTTGTGG 1216
Qy 1024 CCATTGAATCTTTCTGCTATATCGTCCCGAGCTGCCATCTTACAGTGATGACG 1083
Db 1217 CCATTGAATCTTTCTGCTATATCGTCCCGAGCTGCCATCTTACAGTGATGACG 1276
Qy 1084 CACTCAAGGAATCAGCAGCCATGCTAAATAAATGCGTCTACGGCACAGCTTCTTGG 1143
Db 1277 CACTCAAGGAATCAGCAGCCATGCTAAATAAATGCGTCTACGGCACAGCTTCTTGG 1336
Qy 1144 TCCTTATGGTATTAAGTGTATTTATCGGGTACGCTATGTGAACAAAGTTTGGCTCAATTT 1203
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Qy 1204 TCCTGGCCCTGTGCTATGTCCTATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTT 1263
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Qy 1264 TTGCTCTCCACACTTCCCGTCTGCTAGCTGGTAAACCGCACTCTTTTATCAAGACACA 1323
Db 1457 TTGCTCTCCACACTTCCCGTCTGCTAGCTGGTAAACCGCACTCTTTTATCAAGACACA 1516
Qy 1324 TTGAGCTTTGCTTAAAGAACCAAGGAATTAACAACATGACAGTCCCATCAAGTTATGGG 1383
Db 1517 TTGAGCTTTGCTTAAAGAACCAAGGAATTAACAACATGACAGTCCCATCAAGTTATGGG 1576
Qy 1384 GATTCCTCTGTAACCTCGAGTCAATTTTCAATGCGCACCTGTGATGAATACTTTGTTCACA 1443
Db 1577 GATTCCTCTGTAACCTCGAGTCAATTTTCAATGCGCACCTGTGATGAATACTTTGTTCACA 1636
Qy 1444 ATAAGCTCACTTCAATCCAGGCACTTCTGGAATGCGTAGTGGTATAATTACAGAGAATC 1503
Db 1637 ATAAGCTCACTTCAATCCAGGCACTTCTGGAATGCGTAGTGGTATAATTACAGAGAATC 1696
Qy 1504 TTGAGGTAATTAACCTCAAGGAGAGATCATCGAAAGCCCTTCAAGCAATCTTCTG 1563
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Qy 1564 ATGCTTAGGCGAGCTTAACCAATGATATGTTCTTGTGACATCACCCTCTTCAAGC 1623
Db 1757 ATGCTTAGGCGAGCTTAACCAATGATATGTTCTTGTGACATCACCCTCTTCAAGC 1816
Qy 1624 TTCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGCTGGAATCAACAGATCTG 1683
Db 1817 TTCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGCTGGAATCAACAGATCTG 1876
Qy 1684 GAGATCTGAAGATGCTCAGAGTCTATTTCCGATTTGGTACTATCTTGCCTATCTGACCA 1743
Db 1877 GAGATCTGAAGATGCTCAGAGTCTATTTCCGATTTGGTACTATCTTGCCTATCTGACCA 1936
Qy 1744 CCTCCTTTGTTTATTAAGCAATGTTGCTTTTGGTGATGATTAAGAGGGTGTTC 1803
Db 1937 CCTCCTTTGTTTATTAAGCAATGTTGCTTTTGGTGATGATTAAGAGGGTGTTC 1996
Qy 1804 TCAGAGACAAGTTCCGTGATGCTGTAAGGTAATTTGCTGTAGGCACTTATCTTGGC 1863
Db 1997 TCAGAGACAAGTTCCGTGATGCTGTAAGGTAATTTGCTGTAGGCACTTATCTTGGC 2056
Qy 1864 CATCCCCATGGGTGATTTGTTATTTGGCTCTCTTTTCAACATGTTGGGCTGGACTTCAGA 1923
Db 2057 CATCCCCATGGGTGATTTGTTATTTGGCTCTCTTTTCAACATGTTGGGCTGGACTTCAGA 2116
Qy 1924 GCCTCAGAGTGCACCGAGGCTGTACAAGCTATTTGCCAAGATTAACATCAACGTTTC 1983
Db 2117 GCCTCAGAGTGCACCGAGGCTGTACAAGCTATTTGCCAAGATTAACATCAACGTTTC 2176
Qy 1984 TGAGGGTTTTGGCCACAGCAAGCCATGGGAACCTTACCTGGGCTTTACTTCAACTG 2043
Db 2177 TGAGGGTTTTGGCCACAGCAAGCCATGGGAACCTTACCTGGGCTTTACTTCAACTG 2236

Qy 2044 CTGCCATTTGCAGAGCTTGGAAATACATCATTTGGCTCCCTGGAATCTTGTGGCCCCAATCTTTT 2103
Db 2237 CTGCCATTTGCAGAGCTTGGAAATACATCATTTGGCTCCCTGGAATCTTGTGGCCCCAATCTTTT 2296
Qy 2104 CCATGTTTTTCTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGGCAAAATTAAC 2163
Db 2297 CCATGTTTTTCTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGGCAAAATTAAC 2356
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Qy 2224 GAATGAGTATCTGCTGCTCTGATGTTTCAATTTCTTCTGTTATTTATGCTATTTAGCCCA 2283
Db 2417 GAATGAGTATCTGCTGCTCTGATGTTTCAATTTCTTCTGTTATTTATGCTATTTAGCCCA 2476
Qy 2284 TGGTAATAGCTGGTATGATCTACAGTACATTTGAATACCAAGGAGCTGAGAAAGATGGG 2343
Db 2477 TGGTAATAGCTGGTATGATCTACAGTACATTTGAATACCAAGGAGCTGAGAAAGATGGG 2536
Qy 2344 GTGATGGTATCCGTGGGCTGTCCCTCAGTCAGGAGCCCGGTTTGTCTTGTCTCGATTTGGAGG 2403
Db 2537 GTGATGGTATCCGTGGGCTGTCCCTCAGTCAGGAGCCCGGTTTGTCTTGTCTCGATTTGGAGG 2596
Qy 2404 AAGGACCTCCACACACTAAAAACTTGGAGCCCTCAGTTGCTTGTATTTACTGAAACTAGATG 2463
Db 2597 AAGGACCTCCACACACTAAAAACTTGGAGCCCTCAGTTGCTTGTATTTACTGAAACTAGATG 2656
Qy 2464 AAGACTTACATGTCAAGCATCTCGCCCTCTCAGCTTTCCTCAGCTCAAGCTCAAGCAGGAA 2523
Db 2657 AAGACTTACATGTCAAGCATCTCGCCCTCTCAGCTTTCCTCAGCTCAAGCAGGAA 2716
Qy 2524 AAGGTTTCACTATTGTGGGCTGTGTCGTTGGGNACTTCTCTAGAGAACTACGCTGAAG 2583
Db 2717 AAGGTTTCACTATTGTGGGCTGTGTCGTTGGGNACTTCTCTAGAGAACTACGCTGAAG 2776
Qy 2584 CTTTAGCTGCTGAGCAGACCATAAAGCACTTAATGGAGGCAAGAGTAAAGGATTTCT 2643
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Qy 2704 GCCTTGGGGGATGAAGCACAACACCGTGGTGGTGGCTTAATGGCTGGCGTCAAA 2763
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Qy 2764 GCGAAGATGCCCGCGCTTGGAAAGACTTTTATTTGGCAGAGTTTCGAGTGAACAATGCTGCC 2823
Db 2957 GCGAAGATGCCCGCGCTTGGAAAGACTTTTATTTGGCAGAGTTTCGAGTGAACAATGCTGCC 3016
Qy 2824 ATCTTGACCTGCTGGTGCTTAAACATCTCCTTTTCCAGCAATGTGGAGCAATTTT 2883
Db 3017 ATCTTGACCTGCTGGTGCTTAAACATCTCCTTTTCCAGCAATGTGGAGCAATTTT 3076
Qy 2884 CTGAGGGCAACATTTGATGTTGGTGGATTTGTGATGATGGGGGATGCTTATGCTACTAC 2943
Db 3077 CTGAGGGCAACATTTGATGTTGGTGGATTTGTGATGATGGGGGATGCTTATGCTACTAC 3136
Qy 2944 CATTTCTACTGAAACAGCAACAGGTGTGGGAAAGTGCAGATACGGATCTTTCACAGTAG 3003
Db 3137 CATTTCTACTGAAACAGCAACAGGTGTGGGAAAGTGCAGATACGGATCTTTCACAGTAG 3196
Qy 3004 CCCAATTTAGAAAGCAACAGTATCCAAATGAAGAGGACCTTAGCCACCTTCTATATCACT 3063
Db 3197 CCCAATTTAGAAAGCAACAGTATCCAAATGAAGAGGACCTTAGCCACCTTCTATATCACT 3256
Qy 3064 TACCCATTTAGGGCGGAGTAGAAGTGTGGAGATGATGACAGTATATATCAGCATATA 3123
Db 3257 TACCCATTTAGGGCGGAGTAGAAGTGTGGAGATGATGACAGTATATATCAGCATATA 3316

Query Match				85.9%;	Score 3657.8;	DB 9;	Length 3674;
Best Local Similarity				99.9%;	Pred. No. 0;		
Matches 3670;				Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
QY	573	GAGGAAGAAATGGACACAGACCGAAGGTGTCTCCCTCCTCAACCGCATGCGCAATTAC	632				
DB	1	GAGGAAGAAATGGACACAGACCGAAGGTGTCTCCCTCCTCAACCGCATGCGCAATTAC	60				
QY	633	ACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGGCGAGAAAAATCACTGAAGGGAAA	692				
DB	61	ACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGGCGAGAAAAATCACTGAAGGGAAA	120				
QY	693	AAGAGCCCAACAGACCCCAATGGGTACTTTCATGGGTGTCTACCTCCCATGTCTA	752				
DB	121	AAGAGCCCAACAGACCCCAATGGGTACTTTCATGGGTGTCTACCTCCCATGTCTA	180				
QY	753	CAAAATATTTTGGAGTGATCTTTTTTATAGCCCTTACATGGGTGGTGCGACAGCTGGA	812				
DB	181	CAAAATATTTTGGAGTGATCTTTTTTATAGCCCTTACATGGGTGGTGCGACAGCTGGA	240				
QY	813	GTTCTTCAGGCTTTTGCAATGTCTTATCTGCTGCTGTGTACAATGTTGACTGCTATC	872				
DB	241	GTTCTTCAGGCTTTTGCAATGTCTTATCTGCTGCTGTGTACAATGTTGACTGCTATC	300				
QY	873	TCCATGAGTGCCATTGGCCACTAATGGAGTGGTGCCAGCTGGGGCTCATACTTTATGATT	932				
DB	301	TCCATGAGTGCCATTGGCCACTAATGGAGTGGTGCCAGCTGGGGCTCATACTTTATGATT	360				
QY	933	TCCGGGCACTGGGCGCAGAGTTTGGTGGGGCTGTGGCCCTCTGCTTTATCTTCGGTACC	992				
DB	361	TCCGGGCACTGGGCGCAGAGTTTGGTGGGGCTGTGGCCCTCTGCTTTATCTTCGGTACC	420				
QY	993	ACATTTGCGAGCGCATGTACATCTTGGTGCCATTGAAATCTTTCTGGTCTATATCGTC	1052				
DB	421	ACATTTGCGAGCGCATGTACATCTTGGTGCCATTGAAATCTTTCTGGTCTATATCGTC	480				
QY	1053	CCCCGAGCTGCGCATCTTTTCAAGTGATGACGCACTCAAGGAATCAGAGCCATGCTAAAT	1112				
DB	481	CCCCGAGCTGCGCATCTTTTCAAGTGATGACGCACTCAAGGAATCAGAGCCATGCTAAAT	540				
QY	1113	AACATGCGTGCTACGGCACAGCTTCTTGGTCTTATGGTATTAGTGGTATTATCGGC	1172				
DB	541	AACATGCGTGCTACGGCACAGCTTCTTGGTCTTATGGTATTAGTGGTATTATCGGC	600				
QY	1173	GTACGCTATGTGAACAAGTTTGGCTCANTTTTCTGGCCGTGTGTCAATTTGTCCATCTTG	1232				
DB	601	GTACGCTATGTGAACAAGTTTGGCTCANTTTTCTGGCCGTGTGTCAATTTGTCCATCTTG	660				
QY	1233	GCCATCTATGCTGGAGCCATCAAGTCTTCTTTTGTCTCCTCCACACTTCCCGGTCTGCATG	1292				
DB	661	GCCATCTATGCTGGAGCCATCAAGTCTTCTTTTGTCTCCTCCACACTTCCCGGTCTGCATG	720				
QY	1293	CTGGGTAACCGCACTCTTTCATCAAGACACATTTGAGCTTGTCTTAAGACCAAGGAATT	1352				
DB	721	CTGGGTAACCGCACTCTTTCATCAAGACACATTTGAGCTTGTCTTAAGACCAAGGAATT	780				
QY	1353	AACAACTGACAGTCCCATCAAAAGTTATGGGATTTCTTCTGTAACCTCGAGTCAATTTTTTC	1412				
DB	781	AACAACTGACAGTCCCATCAAAAGTTATGGGATTTCTTCTGTAACCTCGAGTCAATTTTTTC	840				
QY	1413	AATGCCACTGTGATGAATATCTTTGTTTCAAAATAAGTCACTTCAATCCAGGGCAATTCCT	1472				
DB	841	AATGCCACTGTGATGAATATCTTTGTTTCAAAATAAGTCACTTCAATCCAGGGCAATTCCT	900				
QY	1473	GGATTGGCTAGTGGTAAATTTACAGAGAAATCTTTGGAGTAATTAACCTACCCAGGGAGAG	1532				
DB	901	GGATTGGCTAGTGGTAAATTTACAGAGAAATCTTTGGAGTAATTAACCTACCCAGGGAGAG	960				
QY	1533	ATCATCGAAAAGCCTTCAGCCAAATCTTCTGATGTCTTTAGGAGCTTTAAACCATGAATAT	1592				
DB	961	ATCATCGAAAAGCCTTCAGCCAAATCTTCTGATGTCTTTAGGAGCTTTAAACCATGAATAT	1020				
QY	1593	GTTCTTGTGTGACATCAACCACTCTCTCACGCTTCTGGTGGGAAATCTTCTTCTCCCTCTGTT	1652				

DB	1021	GTCTTGTGTGATCATCACCACTCTCTTACGCTTCTGGTGGGAATCTTCTTCTCCCTCTGTT	1080
QY	1653	ACAGGTATCATGGCTGGATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAAAGTCTATT	1712
DB	1081	ACAGGTATCATGGCTGGATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAAAGTCTATT	1140
QY	1713	CCGATTGGTATATCTCTTGGCCATCTGACACCTCTCTTGTGTTATTTAAGCAATGTGTC	1772
DB	1141	CCGATTGGTATATCTCTTGGCCATCTGACACCTCTCTTGTGTTATTTAAGCAATGTGTC	1200
QY	1773	CTTTTGGTGCATGTATTGAAGGGGTCTCTCAGAGACAAGTTCGGTGTGCTGTGAAA	1832
DB	1201	CTTTTGGTGCATGTATTGAAGGGGTCTCTCAGAGACAAGTTCGGTGTGCTGTGAAA	1260
QY	1833	GCTAATTTGGTGTAGGCACTTATCTTGGCCATCCCCATGGGTGATTGTTATTGGCTCC	1892
DB	1261	GCTAATTTGGTGTAGGCACTTATCTTGGCCATCCCCATGGGTGATTGTTATTGGCTCC	1320
QY	1893	TTCTTTTCAACATGTGGGGCTGGACTTTCAGAGCCTTCAAGTGCAACCGAGGCTGTACAA	1952
DB	1321	TTCTTTTCAACATGTGGGGCTGGACTTTCAGAGCCTTCAAGTGCAACCGAGGCTGTACAA	1380
QY	1953	GCTATTGCGAAGGATACATCATACCGTCTTCTGAGGGTTTTTGGSCACAGCAAGCCCAAT	2012
DB	1381	GCTATTGCGAAGGATACATCATACCGTCTTCTGAGGGTTTTTGGSCACAGCAAGCCCAAT	1440
QY	2013	GGGGAACCTACTCGGGCTTTACTTCTAACTGCTGCAATTCAGAGCTTGGGAATACTCAAT	2072
DB	1441	GGGGAACCTACTCGGGCTTTACTTCTAACTGCTGCAATTCAGAGCTTGGGAATACTCAAT	1500
QY	2073	GCCTCCCTGGATCTTGTGGCCCCCAATCTTTTCCATGTTTCTCATGTGTTACCTCTTT	2132
DB	1501	GCCTCCCTGGATCTTGTGGCCCCCAATCTTTTCCATGTTTCTCATGTGTTACCTCTTT	1560
QY	2133	GTAAACTTGGCATGTGCTTGCCTGCAACATTAATCTTGAACACCCCACTGAGAGACCCGATTC	2192
DB	1561	GTAAACTTGGCATGTGCTTGCCTGCAACATTAATCTTGAACACCCCACTGAGAGACCCGATTC	1620
QY	2193	CGCTACTACCAATTTGGGCCCTTCTTCTCATGGGAATGAGTATCTGTCTGGCTCTGATGTTTC	2252
DB	1621	CGCTACTACCAATTTGGGCCCTTCTTCTCATGGGAATGAGTATCTGTCTGGCTCTGATGTTTC	1680
QY	2253	ATTTCTTCTGGTATTAATGCAATTTAGCCATGGTAATAGCTGGTATGATCTTACAAGTAC	2312
DB	1681	ATTTCTTCTGGTATTAATGCAATTTAGCCATGGTAATAGCTGGTATGATCTTACAAGTAC	1740
QY	2313	ATTGAATACCAAGAGCTGAGAAAGATGGGGTGAATGGTATCCGTGGGCTGTCCCTCAGT	2372
DB	1741	ATTGAATACCAAGAGCTGAGAAAGATGGGGTGAATGGTATCCGTGGGCTGTCCCTCAGT	1800
QY	2373	GCAGCCGGTTTGTCTTTCGATTTGGAGGAAGACCTCCACACACTTAAACACTGGAGG	2432
DB	1801	GCAGCCGGTTTGTCTTTCGATTTGGAGGAAGACCTCCACACACTTAAACACTGGAGG	1860
QY	2433	CCTCAGTTGCTGTATTACTGAAACTAGATGAAGACTTACATGTCAAGCACTCTCGCCTC	2492
DB	1861	CCTCAGTTGCTGTATTACTGAAACTAGATGAAGACTTACATGTCAAGCACTCTCGCCTC	1920
QY	2493	CTCAGCTTTCCTCAGAGCTCAAGAGGAAAGGTTTCACTATTGTGGGCTCTGTGATC	2552
DB	1921	CTCAGCTTTCCTCAGAGCTCAAGAGGAAAGGTTTCACTATTGTGGGCTCTGTGATC	1980
QY	2553	GTGGGGAACCTCTAGAGAACTACGGTGAAGCTTTTACTGCTGAGAGACCATTAAGCAC	2612
DB	1981	GTGGGGAACCTCTCTAGAGAACTACGGTGAAGCTTTTACTGCTGAGAGACCATTAAGCAC	2040
QY	2613	CTAATGAGGAGCAGAGAGGTAAAGGATTCTGCCAGCTGGTGGTGGCGCCCAAGCTGAGA	2672
DB	2041	CTAATGAGGAGCAGAGAGGTAAAGGATTCTGCCAGCTGGTGGTGGCGCCCAAGCTGAGA	2100
QY	2673	GAGGCAATTTCCCACTCTCATCCAGTCAATGTGGCTTCTGGGGCATGAAGCAACACCGGTG	2732

Db 2101 GAGGGGATTTCCTCACTCACTCAGTCACTGTCGCTTGGGGGATGAAGCACAACACGGTG 2160
Qy 2733 GTGATGGCTGGCTTAATGGCTGGCTCAAGCGAAGATGCCCGCGCTTGGAGACTTTT 2792
Db 2161 GTGATGGCTGGCTTAATGGCTGGCTCAAGCGAAGATGCCCGCGCTTGGAGACTTTT 2220
Qy 2793 ATTGGCACAGTTTCGAGTGACAATGCTGCTGCCATCTTTGCACTCTCTGGTGGCTAAACATC 2852
Db 2221 ATTGGCACAGTTTCGAGTGACAATGCTGCTGCCATCTTTGCACTCTCTGGTGGCTAAACATC 2280
Qy 2853 TCCTCTTTCCAGCAATGTGAGCAATTTTCTGAGGGCAACATTTGATGTGTGGTGGATT 2912
Db 2281 TCCTCTTTCCAGCAATGTGAGCAATTTTCTGAGGGCAACATTTGATGTGTGGTGGATT 2340
Qy 2913 GTGCATGATGGGGGATGCTTATGCTACTACCATCTTCTACTGAAACAGCACAGGTGTGG 2972
Db 2341 GTGCATGATGGGGGATGCTTATGCTACTACCATCTTCTACTGAAACAGCACAGGTGTGG 2400
Qy 2973 CGAAGTGCAGCATACGAGTCTTTCACAGTAGCCCAATTTAGAAGACAACAGTAGTCCAAATG 3032
Db 2401 CGAAGTGCAGCATACGAGTCTTTCACAGTAGCCCAATTTAGAAGACAACAGTAGTCCAAATG 2460
Qy 3033 AGAAGGACTAGCCACCTTCTATATCACTTACGCAATGAGCGGAGTAGAAGTGTG 3092
Db 2461 AGAAGGACTAGCCACCTTCTATATCACTTACGCAATGAGCGGAGTAGAAGTGTG 2520
Qy 3093 GAGATGCATGACAGTGATATATCAGCATATCTTACGAGCGCACTTTGATGATGGAACAA 3152
Db 2521 GAGATGCATGACAGTGATATATCAGCATATCTTACGAGCGCACTTTGATGATGGAACAA 2580
Qy 3153 AGGTCCAGATGCTTCGGCACATGCGGCTATCCAAACAGAGCGAGACAGAGGCGACAA 3212
Db 2581 AGGTCCAGATGCTTCGGCACATGCGGCTATCCAAACAGAGCGAGACAGAGGCGACAA 2640
Qy 3213 TTGGTGAAGACCGAACTCAATCTACGATGACAGCATTTGGCTCTGATGAGACGAA 3272
Db 2641 TTGGTGAAGACCGAACTCAATCTACGATGACAGCATTTGGCTCTGATGAGACGAA 2700
Qy 3273 GAGACAGAACTTATCAGGAGAGGTGCACATGACTTTGACAAAAGACAGATACATGGCA 3332
Db 2701 GAGACAGAACTTATCAGGAGAGGTGCACATGACTTTGACAAAAGACAGATACATGGCA 2760
Qy 3333 TCCGGGGACAAAAGCGAAGTCAATGGAAGATTCCAGGACCTGCTTAACATGCGTCCG 3392
Db 2761 TCCGGGGACAAAAGCGAAGTCAATGGAAGATTCCAGGACCTGCTTAACATGCGTCCG 2820
Qy 3393 GACCACTCAATGTGAGGCGGATGCATACAGCAGTGAACCTCAACAGGTATTAGTTAAC 3452
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ACCESSION AF108831
VERSION AF108831.1 GI:4585228

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Hiki,K., D'Andrea,R.J., Furze,J., Crawford,J., Woollatt,E.,
Sutherland,G.R., Vadas,M.A. and Gamble,J.R.
Cloning, characterization, and chromosomal location of a novel
human K+-Cl- cotransporter
J. Biol. Chem. 274 (15), 10661-10667 (1999)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Hiki,K., D'Andrea,R.J., Sutherland,G.R., Vadas,M.A. and Gamble,J.
Direct Submission
Submitted (23-NOV-1998) Human Immunology, Hanson Centre for Cancer
Research, Frome Road, Adelaide, South Australia 5000, Australia

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DB	529	GTGGTGGGCACAGCTGGAGTCTCTCAGGCTTTTGGCAATTTGCTTATCTGCTGCTGTGT	588
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QY	1275	CACCTCCCGGTCTGATGCTGGGTAAACCGCATCTTTTCTCAAGACACATTCAGCTTTC	1334
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DB	1429	GATGCTCAGAAAGTCTATTCCGATTTGGTACTATCTTGTGCATCTCAGCACCTCTCTTGT	1488
QY	1755	TATTAAAGCAATGTGCTCTTTTGGTGCATGTATTGAAGGGTGTGTTCTCAGAGACAAG	1814
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QY	1815	TTGGTGTGCTGAAAGGTAAATTTGGTGTAGGCACCTTATCTTGGCCATCTCCCATGG	1874
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DB	1669	GCACCGGCTGCTACAGCTATTGCCAAGGATAACATCATACCGTTTCTGAGGGTTTT	1728
QY	1995	GGCCACAGCAAGCCAAATGGGGAACCTTACCTGGGCTTTTACTTCACTGCTGCCATTCGA	2054
DB	1729	GGCCACAGCAAGCCAAATGGGGAACCTTACCTGGGCTTTTACTTCACTGCTGCCATTCGA	1788
QY	2055	GAGCTTGAATACCTATTGCTCCCTGGATCTTGTGGCCCCCAATTTCTTCCATGTTTTT	2114
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AF116242			
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ACCESSION	AF116242		
VERSION	AF116242.1	GI:6693797	
KEYWORDS			
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ORGANISM	Homo sapiens		
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AUTHORS	Race,J.E., Makhlof,F.N., Logue,P.J., Wilson,F.H., Dunham,P.B. and Holtzman,E.J.		
TITLE	Molecular cloning and functional characterization of KCC3, a new K-cl cotransporter		
JOURNAL	Am. J. Physiol. 277 (6 Pt 1), C1210-C1219 (1999)		
MEDLINE	20068487		
PUBMED	10600773		
REFERENCE	2 (bases 1 to 3453)		
AUTHORS	Race,J.E., Makhlof,F.N., Wilson,F.H., Logue,P.J., Dunham,P.B. and Holtzman,E.J.		
TITLE	Direct Submission		

JOURNAL	Submitted (22-DEC-1998) Medicine, SUNY HSC, 750 E Adams St, Syracuse, NY 13210, USA
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RESULT 6

AF211854
LOCUS AF211854 6120 bp mRNA linear ROD 31-JUL-2001
DEFINITION Mus musculus K-Cl cotransporter 3a mRNA, complete cds,
alternatively spliced.
ACCESSION AF211854
VERSION AF211854.1 GI:15042076
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6120)
REFERENCE Pearson, M., Lu, J., Mount, D.B. and Delpire, E.
AUTHORS Localization of the K(+) -Cl(-) cotransporter, KCC3, in the central
TITLE and peripheral nervous systems: expression in the choroid plexus,

JOURNAL MEDLINE
PUBMED 21143254
REFERENCE 11246162
2 (bases 1 to 6120)
AUTHORS Mount, D.B., Song, L.S. and Delpire, E.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1999) Nephrology, Vanderbilt University Medical Center, S-3223 Medical Center North, VUMC, Nashville, TN 37232, USA
FEATURES Location/Qualifiers
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CDS
/note="KCC3a; includes alternative exon 1a; alternatively spliced"

BASE COUNT 1645 a 1425 c 1380 g 1670 t
ORIGIN

Query Match 69.5%; Score 2960.8; DB 10; Length 6120;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 3366; Conservative 0; Mismatches 435; Indels 76; Gaps 7;

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RESULT 7
AF211855
LOCUS
DEFINITION
Mus musculus k-Cl cotransporter 3b mRNA linear ROD 31-JUL-2001
alternatively spliced.
ACCESSION
AF211855
VERSION
AF211855.1 GI:15042078
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Metazoa; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 5964)
Pearson, M.M., Lu, J., Mount, D.B. and Delpire, E.
Localization of the K(+)-Cl(-) cotransporter, KCC3, in the central
and peripheral nervous systems: expression in the choroid plexus,
large neurons and white matter tracts
Neuroscience 103 (2), 481-491 (2001)
21143254
11246162
2 (bases 1 to 5964)
Mount, D.B., Song, L.S. and Delpire, E.
Direct Submission
Submitted (03-DEC-1999) Nephrology, Vanderbilt University Medical
Center, S-3223 Medical Center North, VUMC, Nashville, TN 37232, USA
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CDS

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BASE COUNT 1608 a 1385 c 1347 g 1624 t
ORIGIN
Query Match 64.2%; Score 2735.2; DB 10; Length 5964;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 3123; Conservative 0; Mismatches 405; Indels 76; Gaps 7;
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Db 3231 CCGGAGTCTATCACCATCTATCTTGAGC 3260

RESULT 9

RNU55815
LOCUS
DEFINITION Rattus norvegicus furosemide-sensitive K-Cl cotransporter (KCC1)
ACCESSION U55815
VERSION U55815.1
KEYWORDS GI:1403706
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 3726)
AUTHORS Payne, J.A., Stevenson, T.J. and Donaldson, L.F.

RNU55815 3726 bp mRNA linear ROD 05-JUL-1996
Rattus norvegicus furosemide-sensitive K-Cl cotransporter (KCC1)

TITLE Molecular characterization of a putative K-Cl cotransporter in rat brain. A neuronal-specific isoform
J. Biol. Chem. 271 (27), 16245-16252 (1996)
96279171
8663311
PUBMED
REFERENCE Gillen, C.M., Brill, S., Payne, J.A. and Forbush, B. III.
2 (bases 1 to 3726)
Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family
J. Biol. Chem. 271 (27), 16237-16244 (1996)
96279170
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PUBMED
REFERENCE Payne, J.A.
3 (bases 1 to 3726)
Direct Submission
Submitted (18-APR-1996) John A. Payne, Human Physiology, University of California, School of Medicine, Med. Sci. Bldg. #4138, Davis, CA 95616, USA
JOURNAL

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REFERENCE   2 (bases 1 to 3734)
AUTHORS     Gillen, C.M.
TITLE       Direct Submission
JOURNAL     Submitted (15-APR-1996) Christopher M. Gillen, Cellular and
Molecular Physiology, Yale University School of Medicine, 333 Cedar
St., New Haven, CT 06520, USA
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VERSION AF121118.1 GI:6049052

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REFERENCE

1 (bases 1 to 3764)

Authors Su, W., Shmukler, B.E., Chernova, M.N., Stuart-Tilley, A.K., de

Franceschi, L., Brugnara, C. and Alper, S.L.

Mouse K-Ci cotransporter KCC1: cloning, mapping, pathological

expression, and functional regulation

Am. J. Physiol. 277 (5 Pt 1), C899-C912 (1999)

JOURNAL

MEDLINE 20035026

PUBMED 10564083

REFERENCE 2 (bases 1 to 3764)

Shmukler, B.E. and Alper, S.L.

Direct Submission

Submitted (15-JAN-1999) Molecular Medicine Unit, Beth Israel

Deaconess Medical Center, 330 Brookline Ave., RW-663, Boston, MA

02215, USA

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RESULT 12
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DEFINITION
ACCESSION AF047339
VERSION AF047339.1 GI:3452286
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Molecular identification and expression of erythroid K:Cl cotransporter in human and mouse erythroleukemic cells
JOURNAL Blood Cells Mol. Dis. 24 (1), 31-40 (1998)
MEDLINE 98184935
PUBMED 9516379
REFERENCE 2 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA
REFERENCE 3 (bases 1 to 3775)
AUTHORS Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA
REMARK Sequence update by submitter
COMMENT On Aug 26, 1998 this sequence version replaced gi:2921848.

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RESULT 13

AF047338

LOCUS

DEFINITION Homo sapiens erythroid K:Cl cotransporter (KCC1) mRNA, complete cds.

ACCESSION AF047338

VERSION AF047338.1

KEYWORDS GI:2921846

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3613) Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S. Molecular identification and expression of erythroid K:Cl cotransporter in human and mouse erythroleukemic cells Blood Cells Mol. Dis. 24 (1), 31-40 (1998) 98184935

AUTHORS PUBMED 9516379

REFERENCE 2 (bases 1 to 3613) Pellegriño, C.M., Rybicki, A.C., Musto, S., Nagel, R.L. and Schwartz, R.S. Direct Submission

TITLE Submitted (09-FEB-1998) Medicine-Hematology, Montefiore Medical Center, 111 East 210th Street, Bronx, NY 10467, USA

JOURNAL Location/Qualifiers

FEATURES

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ACCESSION AR270566
VERSION AR270566.1 GI:29701800
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3722)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1129 31-DEC-2002;
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ACCESSION U55054
VERSION 1
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REFERENCE 1 (bases 1 to 3722)
AUTHORS Gillen,C.M., Brill,S., Payne,J.A. and Forbush,B. III.
TITLE Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family
J. Biol. Chem. 271 (27), 16237-16244 (1996)
MEDLINE 96279170
PUBMED 8663127
REFERENCE 2 (bases 1 to 3722)
AUTHORS Gillen,C.M.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1996) Christopher M. Gillen, Cellular and Molecular Physiology, Yale University School of Medicine, 333 Cedar St., New Haven, CT 06520, USA
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ORIGIN
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Best Local Similarity 71.1%; Pred. No. 0;
Matches 2196; Conservative 0; Mismatches 888; Indels 6; Gaps 1;
Qy 536 AGGAGATCAATATTTTGATAAAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACC 595
Db 226 AGGAATTGACTACTATGACAGGACCTGGCACTGTTGAGGAGAGCTGGACATCGGCC 285
Qy 596 GAAGTGTTCTCCCTCTCAACCGCATGGCCAAATTACACTAATCTGACTCAAGAGCAAA 655
Db 286 AAAGTATCGTCTCTCTGGGAAAGCTCGTCAGCTACACCACTCACCCAGGGGCCAA 345
Qy 656 GGAACATGAAGGACGAGAAACATCACTGAAGGAAABAGAGCCCAACACACCCCA 715
Db 346 AGAGCATGAGGAGGCGGAGAGTGGGGAGGGGACCCCGCGGAGGGCAGCGGACCCAG 405
Qy 716 AATGGGTACCTTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCT 775
Db 406 CATGGGACCTTCATGGGGTGTACTGCTCCCTGCTGCAGATACTTTGGGTATCTCT 465
Qy 776 TTTTTCACCCCTTACATCGGTGGTGGGACAGCTGAGGTTCTTACAGGCTTTTGCATTTGT 835
Db 466 CTTCCTCGGCTGACCTGGATGGTGGGACAGAGGTGTGTACAGGCTCTCTCATCTGT 525
Qy 836 CTTTATCTGCTGCTGCTGCTACAAATGTTGACTGTCTATCTCCATGAGTGCCATGCCACTAA 895
Db 526 GCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 585
Qy 896 TGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955
Db 586 CGGTGTGTTCCAGCTGGGGGCTCCTATTTTCATGATCTCTGCTGCTGCTGCTGCTGCT 645
Qy 956 TGGTGGGCTGTGTCCTCTCTGTTTATCTTGGTACCACATTTGAGGAGCCATGTACAT 1015
Db 646 TGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
Qy 1016 CTTTGGTGGCATTGAATCTTCTGCTGCTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1075
Db 706 CTTGGGGGCGCATCGAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765

Db 2925 CTCGGCCCTCGCGCTGGAGAGCCTGTACTCGACGAGGAAGATGAGTCTGCAGTGGGGC 2985
Qy 3290 GGAGAGGTGCACATGACTTGGACAAAAGACAAAGTACATGGCATCCCGGGACAAAAAGC 3349
Db 2986 TGACAAGATCCAGATGACGTGGACGAGGACAAGTACATGACTGAGACCTGGGACCCAG 3045
Qy 3350 GAAGTCAATGGAAGGATTCAGGACCTGCTTAACATGCGTCCGGACCAAGTCCCAATGTGAG 3409
Db 3046 CCATGCCCCGTGACAATTTCCGGGAGCTGGTGACATTAAAGCCGGACCAATCCCAATGTGG 3105
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Qy 3470 GCTGGTTTTTATGAATATCCAGGGCCACCCGAAACCCCTGAGGGTGATGAAACTACAT 3529
Db 3166 CTGGTTCTCCTAAACATGCTGGCCACCCAGGAACAGTGAGGGGACGAGAACTACAT 3225
Qy 3530 GGAGTTCCTAGAGTGCTTACCGAGGAGCTAGAGCGAGTCTTACTTGTCGGGGTGGTGG 3589
Db 3226 GGAGTTCCTGAGGTGCTGACCGAGGGCCTTGAGCGGGTCTGTTGGTGGCGGTGGTGG 3285
Qy 3590 CAGTGAAGTATCACCAATTTATTCATAACC 3619
Db 3286 CCGTGAAGTATCACCAATTTATTCATAACC 3315

Search completed: November 26, 2003, 22:20:38
Job time : 15104 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 26, 2003, 17:43:46 ; Search time 8187 Seconds
(without alignments)
12646.521 Million cell updates/sec

Title: US-09-835-976B-15
Perfect score: 4260
Sequence: 1 tgaatagaagattcttagt.....aaaaaaaaaaaaaaaaaaaaa 4260

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
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6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4129.8	96.9	4584	11 BC033894	BC033894 Homo sapi
2	4048	95.0	5437	11 BC051709	BC051709 Homo sapi
3	3938.8	92.5	4469	11 BC051744	BC051744 Homo sapi
4	726	17.0	738	13 BU623116	BU623116 UI-H-FL1-

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT	
BC033894	Homo sapiens, solute carrier family 12 (potassium/chloride transporters), member 6, clone IMAGE:5269073, mRNA.	BC033894	BC033894.1	GI:21707904	HTC	Homo sapiens (human)	1 (bases 1 to 4584)	Strausberg, R.	Direct Submission	Submitted (02-JUL-2002)	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.nci.nih.gov	Contact: MGC help desk Email: cgabs@emil.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
CB998883	4584 bp mRNA linear HTC 08-JUL-2002	CB998883	CB998883	14	738	14	738	14	738	14	738	14	738
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BI825527	603072276	BI825527	BI825527	12	666	12	666	12	666	12	666	12	666
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CB350003	UI-M-FY0-	CB350003	CB350003	12	666	12	666	12	666	12	666	12	666
CB350624	UI-M-G10-	CB350624	CB350624	12	666	12	666	12	666	12	666	12	666
BE780202	601468080	BE780202	BE780202	12	666	12	666	12	666	12	666	12	666
BG399131	602440606	BG399131	BG399131	12	666	12	666	12	666	12	666	12	666
CB519030	UI-M-GH0-	CB519030	CB519030	12	666	12	666	12	666	12	666	12	666
CD557617	AGENCOURT	CD557617	CD557617	12	666	12	666	12	666	12	666	12	666
BO933903	AGENCOURT	BO933903	BO933903	12	666	12	666	12	666	12	666	12	666
BF104796	601822489	BF104796	BF104796	12	666	12	666	12	666	12	666	12	666
BU703975	UI-M-F00-	BU703975	BU703975	12	666	12	666	12	666	12	666	12	666
BG299180	602395340	BG299180	BG299180	12	666	12	666	12	666	12	666	12	666
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CA324006	UI-M-FY0-	CA324006	CA324006	12	666	12	666	12	666	12	666	12	666
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BG718532	602696594	BG718532	BG718532	12	666	12	666	12	666	12	666	12	666
BI346729	376022 MA	BI346729	BI346729	12	666	12	666	12	666	12	666	12	666
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BG718675	602696792	BG718675	BG718675	12	666	12	666	12	666	12	666	12	666
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BE925767	RC3-BN003	BE925767	BE925767	12	666	12	666	12	666	12	666	12	666
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BI172854	602337292	BI172854	BI172854	12	666	12	666	12	666	12	666	12	666
AK052910	Mus muscu	AK052910	AK052910	12	666	12	666	12	666	12	666	12	666
AI127820	qc36e12.x	AI127820	AI127820	12	666	12	666	12	666	12	666	12	666
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CD505248	CDA72-F08	CD505248	CDA72-F08	12	666	12	666	12	666	12	666	12	666

ALIGNMENTS

RESULT 1
LOCUS BC033894
DEFINITION Homo sapiens, solute carrier family 12 (potassium/chloride transporters), member 6, clone IMAGE:5269073, mRNA.
ACCESSION BC033894
VERSION BC033894.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4584)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs@emil.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>
 contact: amadan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 47 Row: O Column: 6
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
 1. .4584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5269073"
 /tissue_type="Testis"
 /clone_lib="NIH MGC_97"
 /lab_host="DH10B"
 /note="Vector: pBluescript"
 BASE COUNT 1209 a 1124 c 1076 g 1175 t
 ORIGIN

Query Match 96.9%; Score 4129.8; DB 11; Length 4584;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4153; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY	93	TCAAAAGTAGCTAGCGTAAGAGAGAGATTTCGAGGTTCCGCCCACTTTTTTGTCTT	152
DB	427	TCAAAAGTAGCTAGCGTAAGAGAGAGATTTCGAGGTTCCGCCCACTTTTTTGTCTT	486
QY	153	AAAAAGAACAAATGATCTCCAGAAACACCAACCAAGATGGCTTCAGTTCGGTTCATG	212
DB	487	AAAAAGAACAAATGATCTCCAGAAACACCAACCAAGATGGCTTCAGTTCGGTTCATG	546
QY	213	GTGACACCCAGCAAGATCGATGACATTCAGGTTTGTTCAGACACAGTCGGGACNTCAGC	272
DB	547	GTGACACCCAGCAAGATCGATGACATTCAGGTTTGTTCAGACACAGTCGGGACNTCAGC	606
QY	273	TCTCGATCTAGTTCCTCGAGTAAGATTTAGCTCCCGGAAAGCGTGCCTGAAACAAGCCGG	332
DB	607	TCTCGATCTAGTTCCTCGAGTAAGATTTAGCTCCCGGAAAGCGTGCCTGAAACAAGCCGG	666
QY	333	AGTGACCTATGATGATGATGCTGGGGCCACCACTTCGCTGGCAACTCTTCGACTGGAT	392
DB	667	AGTGACCTATGATGATGATGCTGGGGCCACCACTTCGCTGGCAACTCTTCGACTGGAT	726
QY	393	CCACCCAGTGACCGGACTTCTCACCCCGAGGATGTCATCGAGGACCTGAGTCAGAACTCC	452
DB	727	CCACCCAGTGACCGGACTTCTCACCCCGAGGATGTCATCGAGGACCTGAGTCAGAACTCC	786
QY	453	ATCACAGGGGAACACAGCCAACTGTTAGACGACGACATGAAGAAAGCTCGAAATGCTTAT	512
DB	787	ATCACAGGGGAACACAGCCAACTGTTAGACGACGACATGAAGAAAGCTCGAAATGCTTAT	846
QY	513	CTCAATAATCCAAATATGAAGAGAGATGAATATTTTGAATAAAATTTGGCACTCTTT	572
DB	847	CTCAATAATCCAAATATGAAGAGAGATGAATATTTTGAATAAAATTTGGCACTCTTT	906
QY	573	GAGGAAGAAATGACACACGACCGAAGGTGTTCTCCCTCAACCGCATGGCCAAATTAC	632
DB	907	GAGGAAGAAATGACACACGACCGAAGGTGTTCTCCCTCAACCGCATGGCCAAATTAC	966
QY	633	ACTAATCTGATCAAGAGCAAAAGGAACATGAAGAGGACGAAACATCACTGAAGGGAAA	692
DB	967	ACTAATCTGATCAAGAGCAAAAGGAACATGAAGAGGACGAAACATCACTGAAGGGAAA	1026
QY	693	AAGAAGCCCAACGACCCCAAAATGGGTACCTTCATGGGTGTCACCTCCCATGCTCTA	752
DB	1027	AAGAAGCCCAACGACCCCAAAATGGGTACCTTCATGGGTGTCACCTCCCATGCTCTA	1086

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QY	813	GTTCTTACAGGCTTTTGAATTTGCTTATCTGCTGCTGCTGTACAAATGTTACATGCTATC	872
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QY	873	TCCATGATGTCATTTGCCACTTAATGGAGTGGTCCAGCTGGGGCTCATATCTTTATGATT	932
DB	1207	TCCATGATGTCATTTGCCACTTAATGGAGTGGTCCAGCTGGGGCTCATATCTTTATGATT	1266
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QY	993	ACATTTGCAGCAGCATGTATACATCTTGGTGGCATTGAAATCTTTCGTGCTATATCGTC	1052
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QY	1053	CCCCGAGCTGCATCTTTTCACAGTGATGACGCACTCAAGGAATCAGCAGCCATGCTAAAT	1112
DB	1387	CCCCGAGCTGCATCTTTTCACAGTGATGACGCACTCAAGGAATCAGCAGCCATGCTAAAT	1446
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QY	1353	AACAATGACAGTCCCATCAAGTTATGGGATTTCTTCTGTAATCTGAGTCAATTTTTC	1412
DB	1687	AACAATGACAGTCCCATCAAGTTATGGGATTTCTTCTGTAATCTGAGTCAATTTTTC	1746
QY	1413	AATGCCACTGTGATGAATATCTTTTTCACAATAACGTCACCTTCAATCCAGGGCAATCTCT	1472
DB	1747	AATGCCACTGTGATGAATATCTTTTTCACAATAACGTCACCTTCAATCCAGGGCAATCTCT	1806
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DB	1807	GGATTGGCTAGTGGTATTAATTAACAGAAATCTTTGGAGTAATTAACCTACCCAGGGAGAG	1866
QY	1533	ATCATCGAAAGCTTTAGCCCAATCTTCTGATGTTTGGAGCTTAAACCATGAATAT	1592
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QY	1593	GTTCTTGTGATCATCACCACTCTTTCAGCTTCTGGTGGGAATCTTCTTCCCTCTGTT	1652
DB	1927	GTTCTTGTGATCATCACCACTCTTTCAGCTTCTGGTGGGAATCTTCTTCCCTCTGTT	1986
QY	1653	ACAGGTATCTAGGCTGGATCAAAAGATCTGGAGATCTGAAAGATGCTCAGAAATCTATT	1712
DB	1987	ACAGGTATCTAGGCTGGATCAAAAGATCTGGAGATCTGAAAGATGCTCAGAAATCTATT	2046
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DB	2047	CCGATTGGTACTATCTTGGCCATCTGACCACTCTTCTTATTTTATTAAGCAATGTTGTC	2106
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DB	2107	CTTTTGTGTCATGTTGAAGGGTGTGTTCTCAGAGACAAAGTTCGGTGAATCTGTGAAA	2166
QY	1833	GGTAATTTGGTGGTAGGCACTTATCTTTGGCCATCCCCATGGGTGATTTTATGGCTCC	1892

Db 2167 GGTAAATTTGGTGGTAGCACCTTTATCTTGGCCATCCCATGGGTGATTTGTTATGGCTCC 2226
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Db 2227 TTCTTTTCAACATGTGGGCTGGACTTCAGAGCCTCAGAGGTGACCGAGGCTGTACAA 2286
Qy 1953 GCTATTGCCAAGGATAACATCATACGTTTCTGAGGGTTTTGGGCCACAGCAAGCCAAAT 2012
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Qy 2013 GGGGAACCTACCTGGGCTTTACTTCTAAGCTGTCATTTGCAAGCTTGAGAGCTTGGAACTCATTT 2072
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RESULT 2
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 ACCESSION BC051709
 VERSION BC051709.1 GI:30704980
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 5437)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S.D., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, J., Helton, E., Kerteman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 5437)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabps@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, J., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 77 Row: a Column: 13
 This clone has the following problem: frame shifted.

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 /note="vector: pbluescript"

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 ORIGIN

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RESULT 3
BC051744
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DEFINITION BC051744 GI:30704365
ACCESSION BC051744
VERSION BC051744.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4469)
AUTHORS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 1247932
PUBMED 1247932
REFERENCE 2 (bases 1 to 4469)
AUTHORS Strausberg,R.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center., Stanford University School of Medicine, Stanford, CA 94305
```


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 ACCESSION BU623116
 VERSION BU623116.1 GI:23289331
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 1 (bases 1 to 738)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
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 Location/Qualifiers
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) with a modified polylinker; Site 1: EcoR I; Site 2: Not
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 a pool of mRNA obtained from 4 cell lines from grade III
 chondrosarcoma tissues. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into p7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is GAGGTGCGTG. The cell
 lines were provided by Dr. James Martin from the
 University of Iowa.
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 TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
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 BASE COUNT 196 a 131 c 157 g 253 t 1 others
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 Best Local Similarity 99.7%; Pred. NO. 2.4e-101;
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 QY 3637 CTTGACCTGTTTTCTTAAAGGCGCTAGCTCTCCATGGAAGTGCAGCTCATTACTACCA 3696
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RESULT 5
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 DEFINITION AGENCOURT_13659995 NIH_MGC_187 Homo sapiens cDNA clone
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 VERSION CB998883.1 GI:30293403
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 738)
 REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: Clontech Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM18 row: i column: 22
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FEATURES

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5'-CACGGCATATGGCC-3' and 3' adaptor sequence:
5'-ATTTCATGCGGAGCGGCCGACATG-TT(30)BN-3' (where B = A,
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(range 0.5-4.0 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC library."

BASE COUNT 223 a 169 c 187 g 159 t

ORIGIN

Query Match 16.4%; Score 696.6; DB 14; Length 738;
Best Local Similarity 99.2%; Pred. No. 7.5e-97;
Matches 711; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
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LOCUS Homo sapiens, clone IMAGE:4943447, mRNA.
DEFINITION BC035480
ACCESSION BC035480
VERSION BC035480.1 GI:22028104
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3648)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 52 Row: e Column: 9
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: no polyA-tail.
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Qy	1051	TCCCCGAGCTGCCATCTTTACACAGTGATGACGCACCTCAAGGAATCAGCAGCCATGCTAA	1110		
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Qy	1111	ATAACATGCGTGTCTACGGCACAGCTTTCTTGGTCTTATGGTATTAAGTGGTATTTATCG	1170		
Db	2068	ACAATATGCGTGTATATGGGACCATTTCCTGACCTTCATGACCCCTGGTGGTTGTGG	2127		
Qy	1171	GCGTACCTATGTCAAACAAGTTTGCTTCANTTTCTGGGCTGTGTGTCATTTGTCATCT	1230		
Db	2128	GGGTCAAGATGTGAACAAATTTTGCTCGCTTCTCTGGGCTGTGTGATCATCTCCATCC	2187		
Qy	1231	TGGGCATCTATGCTGGAGCCATCAAGTCTCTTTTGTCTCTCCACACTTCCCGTCTGCA	1290		
Db	2188	TCTCCATCTATGCTGGGGGCATAAAGTCTATATTTGACCTTCCGTTTCCGGTATGCA	2247		
Qy	1291	TGCTGGGTAAACCGCACTCTTTTCATCAAGACACATGTGAGTTGCTTAAGACCAAGGAA	1350		
Db	2248	TGCTGGGCAACAGACAGCCCTGTCTCCGGGACACAGTTTGACATCTGTGCAAGACAGCTGTAG	2307		
Qy	1351	TTAACACATGACAGTCCCATCAAGTTATGGGGATCTTCTGTGTA	CTCAGTCAATTTT	1410	
Db	2308	TGGCAATGAGACAGTGGCACCCAGCTATGGAGTTTCTTCTGCCACAGCCCCAACCTTA	2367		
Qy	1411	TCATGCCACCTGTGATGAATACTTTCTTACAAATAACGTCACTTCAATCCAGGGCATTC	1470		
Db	2368	CGACCGACTCTGTGACCCCTACTTTCATGCTCAACATGTGACCGAGATCCCTTGGCATCC	2427		
Qy	1471	CTGATTTGGCTAGTGGTATTAATACAGAGAAATCTTTGGAGTAATACCTACCAAGGAG	1530		
Db	2428	CCGGGGCAGCTGCTGTGTGTCTCCAGGAAACCTGTGGAGCGCTACTCTGGAGAGGGTG	2487		
Qy	1531	AGATC-----ATCGAAAAGCCTTCAGCCCAATCTTCTGATGTCTTAGGCAGCTTAAACCA	1585		
Db	2488	ACATCTGGAGAGCATGGGTGCGCTCCGAGATGCCCCCGAGCTGAAGGAGAGCCTGCC	2547		
Qy	1586	TGAATATGTTCTTGTGACATCACCACTCTTTCACGCTTCTGGTGGGAATCTTCTTTC	1645		
Db	2548	TCTGTACGTGTCGCTGACATCGCCACATCTTTCACCGTCTGGTGGCATCTTCTCCC	2607		
Qy	1646	CTCTGTACAGGTATCATGGCTGGATCAAAACAGATCTGGAGATCTGAAGAGATGCTCAGAA	1705		
Db	2608	TTCTGTAAACAGGCATCATGGCTGGCTCAAAACCGCTCTGGGGACCTTCTGTCAGCAGGAG	2667		
Qy	1706	GTCTATTTCCGATGGTACTACTTCTTGGCATCTCTGACCACTCTCTTGTGTTAT-----	1757		
Db	2668	GTCTATCCCTGTGGGGACCAATCTGGGCCATCTTACAACTTCCCTCTGTGTATCTTTC	2727		
Qy	1758	-----	1757		

Db	2728	CCAGGCCTGGGGCAGGTGGGGCAGAGCAGCGGAAAGCGCTTTGGCGTGTGTACGTTGGCCAGG	278
Qy	1758	-----	1757
Db	2788	TCACATGCACAGACACCCACACACTCATATATAGCTCCCTTCTCATGCACACATGCAC	2847
Qy	1758	-----	1757
Db	2848	ATACACACCAGAGACTCCAGCTGTAGGTGTCTCTGTAGTCTGTGGCTGGGTGGGGGCAC	2907
Qy	1758	-----	1757
Db	2908	GTGGTACTATTACGGGACAGTGGGGTGGCAGAGCCGAGTTTCTTTGACGCCGCCGCAG	2967
Qy	1758	--TTAAGCAATTTGTCTCTTTTGGTGCATGTATTGAAGGGGTTGTCTCTCAGAGACAAAGT	1815
Db	2968	ACTTCAGCAGTGTGGTTCTCTTTGGTGCCTGCATTGAGGGTGTGGTTCTCCGGGACAAGT	3027
Qy	1816	TCGGTGTATGCTGTGAAGAGTAAATTTGGTGTGTAGGCACCTTATCTTGGGCCATCCCCATGGG	1875
Db	3028	ATGGCATGTGTGTGCAGCAGGAACCTTGGTGTGGGCAACACTGGCGCTGGCCTTCACCCCTGGG	3087
Qy	1876	TGATTGTATTGGCTCCTCTCTTTTCAACATGTGGGCTGGACTTCAGAGCGCTCACAGGTG	1935
Db	3088	TCATGTGTATCGGGCTCCTCTCTTTTCAACGTGTGGCGCTGGCCCTCCAGAGCCTCACAGGGG	3147
Qy	1936	CACCGAGGCTGTACAAAGCTATTGCCAAGGATAAACAATCATACCGTTTCTCAGAGGTTTTCG	1995
Db	3148	CACCAGCCTATTGCAGGCCATTGGCCAGAGCAACATCATCCCTTCTCCGGGTGTTCG	3207
Qy	1996	GCCACAGCAAGCCAAATGGGGAACCTACCTGGGCTTTTACTTTAACTGTCTGCCATTGCAG	2055
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Qy	2056	AGCTTGAATACTCATTTGGCTCCTCGATCTTGTGGCCCAATCTTTCCATGTTTTC	2115
Db	3268	AGCTGGGCATCTCATCGCCTCCTCGACATGGTGGCCCCCATCTTATCCATGTTCTTTC	3327
Qy	2116	TCATGTGTTTACCTCTTTGTAAACTTGGCATGTGCCATTGCAAACTTACTTCGAACACCCA	2175
Db	3328	TGATGTCTACCTGTTCTGTGAACCTCGCCTGTGGGTGCAGACACTCCTGAGAGCCCCCA	3387
Qy	2176	ACTGGAGACCCCGATTCCGGCTACTACCATTTGGGCCCTTTCTTTTCATGGGAATCAGTATCT	2235
Db	3388	ACTGGCGCCCCGTTCAAGTACTATCACTGCGCGCTGTCTTCTCTGGGCATGAGTCTCT	3447
Qy	2236	GTCTGGCTCTGATGTTTCAATTTCTTCTCTGTTATTTATGCCATTGTAGCCATGTTAATAGCTG	2295
Db	3448	GCCTGGGCCCTTATGTTTGTCTCTCTCTGTTACTATGCCCTGGTGGGCATGCTCATCGCGG	3507
Qy	2296	GTATGATCTACAAGTACATTGAATATCAAGAGGACTGAGAAAGAAATGGGGTGTGGTATCC	2355
Db	3508	GCATGATCTACAATAATACATCGATACCAAGGGCTGAGAAGGAGTGGGTGACGGGATCC	3567
Qy	2356	GTGGGCTGTCCCTCAGTGCAGCCCGTTTGTCTTTGCTTCGATTGGAGGAGGACCTCCAC	2415
Db	3568	GAGGCTGTCCCTGAGCGCTGCCCGCTACGCGCTGTTGGCGCTGGAGGGGGGSCCTCCTC	3627
Qy	2416	ACACTAAAACCTGGAGGCCTC	2436
Db	3628	ACACCAAGAACTGGCGCGCGC	3648
RESULT 7			
BG776289			
LOCUS			
DEFINITION 602663357F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4808366 5',			
mRNA sequence.			
ACCESSION BG776289			
VERSION BG776289.1 GI:14046606			
KEYWORDS EST.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
FEATURES			
CDS			
ORF			
ORIGIN			
COMMENTS			
BIBL			
REFERENCES			
GENERAL NOTES			
DBLINK			
HISTORY			
CONVERSION			
REMARKS			
PROJECT			
SUBMITTER			
SUBMISSION			
ANALYSIS			
COMPARISON			
ALIGNMENT			
BLAST			
FASTA			
FASTQ			
SRA			
NCBI			
ENR			
PDB			
RCSB			
PDBe			
EMBL			
GenBank			
DDBJ			
EBI			
ENA			
NCBI			
SRA			

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seq primer: m13 reverse
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CK1-afh-e-15-0-UI"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CK1"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site1: EcoR I; Site_2: Not I;
UI-E-CK1 is a normalized cDNA library containing the
following tissue(s): Retina Foveal and Macular. The
library was constructed according to Bonaldo, Lennon and

```


QY 2571 AACTACGGTGAAGCTTTAGCTGCTGAGCAGACATATAAAGCACCTAATGTGAGGCGAGAGAAG 2630
 |||||
 Db 485 AACTATGGTGTAGCGCGCTCCGGCAGAGCAGACCAATTAGCAGCTAATGGAGGCGAGAGAAG 544
 |||||
 QY 2631 GTAAAGAGATTCTGCAGCTGTGTGTGGCCGCAAGCTGAGAGAGGCGCATTTCCACCTTC 2690
 |||||
 Db 545 GTAAAGAGATTCTGCAGATTGGTGGTGGCTGCGCAAGCTGAAAGAGGCGCATATCACACCTTC 604
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 QY 2691 ATCCAGTGTGGCTTGGGGCATGAGCAGACACACAGCTGGTGTGATGGCTGGCTTAAT 2750
 |||||
 Db 605 ATCCAGTGTGGCTTGGGGCATGAGCAGACACACAGCTGGTGTGATGGCTGGCGCCAAT 664
 |||||
 QY 2751 GGCTGGCTGCAAGCGAAGATGCCCGCTTGGAGACTTTTATTGGCAGCTTCGAGTG 2810
 |||||
 Db 665 GGCTGGCTGAGGTGAAGATGCTCGGCTTGGAGACTTTTATTGGCAGCTTCGAGTG 724
 |||||
 QY 2811 ACAACTGTGCCCATCTTGCACCTGTGGTGGCTTAAACATCTCCTTTCTTCC 2863
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 Db 725 ACAACTGTGCCCATCTAGCCCTGTGGTGGCTTAAACATGCTCCTTTCTTCC 777
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RESULT 10

BI825527
 LOCUS 603072276F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164098 5',
 mRNA sequence.

ACCESSION BI825527

VERSION BI825527.1 GI:15937077

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 905)

NIH-MGC <http://imgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11407 row: h column: 19

High quality sequence start: 9

High quality sequence stop: 746.

FEATURES

source

1..905

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5164098"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site:1; NotI;

Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH MGC Library."

BASE COUNT 218 a 233 c 227 g 227 t

ORIGIN

Query Match 14.7%; Score 627.8; DB 12; Length 905;

Best Local Similarity 91.8%; Pred. No. 2.2e-86;

Matches 766; Conservative 0; Mismatches 48; Indels 20; Gaps 9;
 QY 240 CCAGTTTGTGTCAGACACACAGTCCGAGCTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATT 299
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 Db 71 CAAGTTTGTGTCAGACACACAGTCCGAGCTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATT 130
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 QY 300 AGCTCCCGGGAAGCGTGCCTGA--AACAGCCGGAGTGAGCCTATGAGTGAGATGCTGG 358
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 Db 131 AGCTCCCGGGAAGCGTGCCTGATAACAAGCCGGAGTGAGCCTATGAGTGAGATGCTGG 190
 |||||
 QY 359 GGCACACACTTCGCTGGCAACTGTGTGACTG-GATCCACCCAGTGACCGGACTTCTCACC 417
 |||||
 Db 191 GGCACACACTTCGCTGGCAACTGTGTGACTGCTCCACCCAGTGACCGGACTTCTCACC 250
 |||||
 QY 418 CCCAGAGTGTCTATCGAGGACCTGAGTCAGAACTCCATCACAGGGGAACACAGCCCACTGT 477
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 Db 251 CCCAGAGTGTCTATCGAGGACCTGAGTCAGAACTCCATCACAGGGGAACACAGCCCACTGT 310
 |||||
 QY 478 TAGACGCGGACATATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAAATTATGAAGAAG 537
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 Db 311 TAGACGCGGACATATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAAATTATGAAGAAG 370
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 QY 538 GAGATGAATATTTTGAATAAAAAATTTGGCACTCTTTGAGGAAGAAATGACACACACCGA 597
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 Db 371 GAGATGAATATTTTGAATAAAAAATTTGGCACTCTTTGAGGAAGAAATGACACACACCGA 430
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 QY 598 AGGTGTCTTCCCTCTCTCAACCGCATGGCCAAATACACTAACTGACTCAAGGAGCAAGAGG 657
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 Db 431 AGGTGTCTTCCCTCTCTCAACCGCATGGCCAAATACACTAACTGACTCAAGGAGCAAGAGG 490
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 QY 658 AACATGAAGAGCGCAGAAAAACATCACTGAAGGGAAAAAGAGCCCAACCAAGACCCCAAAA 717
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 Db 491 AACATGAAGAGCGCAGAAAAACATCACTGAAGGGAAAAAGAGCCCAACCAAGACCCCAAAA 550
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 QY 718 TGGGTACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCCTTT 777
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 Db 551 TGGGTACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCCTTT 610
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 QY 778 TTTTACGCTTTACATGGGTGGTGGGCACAGC-TGGAGTTCTTCAGGCTTTTGC-AATTGT 835
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 Db 611 TTTTACGCTTTACATGGGTGGTGGGCACAGCTTGGAGTTCTTCAGGCTTTTGC-AAATTGT 670
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 QY 836 CTTTATCTGCTGCTGTACAAATTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTAA 895
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 Db 671 CTTTATCTGCTGCTGTACAAATTTGACTGTCTATCTCCATGAGTGCCATTTGGCACAATA 730
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 QY 896 --TGGAGTGGTCCAGCTGGGGGCTCACTACT-----TTATGATTTCCCGGGCACTGGG 946
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 Db 731 ATGGGAGTGGTCCAGCTGGGGGCTCACTACTCTAATGAATTTCCGTCGACCTGGG 790
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 QY 947 CCCAGAGTTTGG--TGGGGCTGTTGGCCTCTGCTTTTATCTTTGGTACACACTTT--GCA 1001
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 Db 791 CCCAGAGTAGGTTGGGGCTTGGACCTCTGCTTTTATCTTTGGTACACACTTTTGGCAG 850
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 QY 1002 CGAGCCATGTACATCTTTGGTGCCATT--GAAATCTTTTGGTCTATATCGTCC 1053
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 Db 851 CGGCAATGTTTCATCACTGGGTGGCTTTGAAAAATCTTCTGGGCTCTATATCGTCC 904
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RESULT 11

CA325003

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 723)

NIH-MGC <http://imgc.ncl.nih.gov/>.

CA325003 723 bp mRNA linear EST 26-NOV-2002

UI-M-FY0-ccm-1-01-0-UI_r1 NIH_BMAP_FY0 Mus musculus cDNA clone

IMAGE: 6821618 5', mRNA sequence.

CA325003

CA325003.1 GI:24543101

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NIH-MGC <http://imgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Query Match	14.5%	Score 619;	DB 14;	Length 723;
Best Local Similarity	91.0%;	Pred. No. 5.5e-85;		
Matches 658;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;
QY	2611	ACCTAATGGAGGCAGAGAAAGGTAAAGGATTCTGCACGTGTGTGTGCGCCGCAAGCTGA	2670	
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QY	1	ACCTAATGGAGGCAGAGAAAGGTAAAGGATTCTGCCAATTGGTGTGTGCTGCCAAGCTGA	60	
DB				
QY	2671	GAGAGGGCATTTCCCACTCTCATCCAGTCATGTGSCCTTGGGGGCATCAAGCAACAACACGG	2730	
DB				
QY	61	AAGAGGGCATTTCAACCTCATCACTCTGTGGCCTCGGAGGCATGAACAACAACACAG	120	
DB				
QY	2731	TGTTGATGGGCTGGCCCTTAATGGCTGGCGTCAAAAGCGAAGATGCCCGCGCTTGGAAAGACTT	2790	
DB				
QY	121	TGTTGATGGGCTGGCCCAATGGCTGGCGTCAGAGTGAAGATGCTCGCGCTTGGNAGACTT	180	
DB				
QY	2791	TTAATGGCAGATTTCAGAGTGACAACTGTCTGCCATCTTTGCACCTGCTGGTGGCTTAAAAAACA	2850	
DB				
QY	181	TCATTGGCAGATACGAGTGACAACTGCTGCCATCTAGCCCTGCTGGTGGCTTAAAAATG	240	
DB				
QY	2851	TCCTCTCTTTCCAGCAATGTGGAGCAATTTCTGAGGGCCACATTGATGTGTGGTGA	2910	
DB				
QY	241	TCCTCTCTTTCCAGCAATGTGGAGCAGTTTCTGAGGGGCAACATTGATGTGTGGTGA	300	
DB				
QY	2911	TTGTGCATGATGGGGGATGCTTATGCTACTACCATTCCTACTGAAACAGCAACAAGTGT	2970	
DB				
QY	301	TTGTGCATGATGGGGCATGCTCATGTATTAACGTTCTCTGCTGAAACAGCAACAAGTTTT	360	
DB				
QY	2971	GGCGAAAGTGCAGCATACGGATCTTCAAGTAGCCCAATTTAGAGAGCAACAGTATCCAAA	3030	
DB				

Db	361	GGCGGAAATGCAGCATACGGATCTTCCACAGTAGCCCAACTAGAGAACAACAGTATTCAGA	420
Qy	3031	TGAAGAAGGACCTAGCACCTTCTTATATCATTACGCCATTACGCCGCGAGGTAGAAGTGG	3090
Db	421	TGAAGAAGGATCTGGCCACCTTTCTGTACCACCTGCGCATTTAGGCGAGAAGTGGAAGTGG	480
Qy	3091	TGAGATGCAATGACAGTGTATATATCAGCATATATACTTTACGAGCCCATCTTTGATGATGAAC	3150
Db	481	TGAGATGTCACGACAGTGCATATCTTGCCTATACATATGAGCGCACCTCTGATGATGAGC	540
Qy	3151	AAGGTCCTCAGATGCTTCGGCACATGCGGCTATCCAAAACAGAGCGACAGAGAGGCGAC	3210
Db	541	AGAGGTCCTCAGATGCTTCGGCATATGCGGCTGTCAAACACAGAGCGAGAGGAGGCGAC	600
Qy	3211	AATTGCTGAAAGACCCGAAACTCAATCTACGATTGACACGATTTGGCTCTGATGAGGACG	3270
Db	601	AGCTGCTGAAGATCGAACTCAATGCTACGCTTGACACGATTTGGCTCTGATGAGGACG	660
Qy	3271	AGAGACAGAAACCTATCAGGAGAAGGTGCATGACTTTGGACAAAAGACAAGTACATGG	3330
Db	661	NAGAGACAGAAACGTAACAGGAGAGGTGCATGACTTTGGACCAAAGGATAAATAATACATGG	720
Qy	3331	CAT 3333	
Db	721	CAT 723	
RESULT 12			
CD350624			
LOCUS			
DEFINITION	CD350624 719 bp mRNA linear EST 29-MAY-2003		
ACCESSION	UI-M-GIO-cgg-m-22-0-UI.r1 NIH BMAP_GIO Mus musculus cDNA clone		
VERSION	IMAGE: 6853151 5', mRNA sequence.		
KEYWORDS	CD350624.1 GI:31142139		
SOURCE	EST.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 719)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: pYX-5. Location/Qualifiers 1..719 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE: 6853151" /tissue_type="whole brain" /dev_stage="embryo 13.5,14.5,16.5,17.5dpc" /lab_host="DH10B (TI phase resistant)" /note="lib=NIH_BMAP_GIO" /note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned		
FEATURES			
source			

directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 146 a 192 c 164 g 216 t 1 others
ORIGIN

Query Match 14.0%; Score 597; DB 14; Length 719;
Best Local Similarity 89.3%; Pred. No. 1.3e-81;
Matches 642; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 743 CCCATGCTACAAATATTTTGGAGTGATCTCTTTTACGCCCTACATGGGTGGG 802
DB 1 CCCATGCTACAGAACATCTTTGGAGTGATCTCTCTCCGCTTACCTGGGTAGTGG 60
QY 803 CACAGCTGGAGTTCTTCAGGCTTTTGCATTTGCTCTTATCTCTGCTGTGTACAAATGTT 862
DB 61 AACAGCTGGAATCCTTCAGGCTTTTGCATTTGCTCTTATCTCTGCTGTGTACAAATGTT 120
QY 863 GACTGCTATCTCATGAGTGCCATGTCCTAATAGAGTGTGTCAGCTGGGGGTCTATA 922
DB 121 AACTGCCATCTCATGAGGCCATCGCCACTAACCGAGTGTGTCAGCTGGGGGTCTATA 180
QY 923 CTTTATGATTTCCGGGCACTGGGCCAGAGTTTGGTGGGGCTGTGGCCTCTGCTTTTA 982
DB 181 CTTTCATGATTTCCAGAGCCCTGGGCCAGAGTTTGGGGGGCTGTAGGGCTCTGCTTTTA 240
QY 983 TCTTGTGTACCAATTTGCAGCAGCCATGTACATCTCTTGGTGCAATTTGTAATCTTTCTGT 1042
DB 241 TCTTGCACCAATTTTGCAGGCGCATGTATCTTGTGGCATTTGTAATCTTTCTGT 300
QY 1043 CTATATCGTCCCGAGCTGCCATCTTTACAGTATGACGCACTCAAGAAATCAGCAGC 1102
DB 301 ATACATTTGTCCCGAGCTGCCATCTTTCGAGTGACGATGCACTCAAGGAGTCAGCAGC 360
QY 1103 CATGCTAAATACATCGCTGTCTACGGCAGCTTTCTTGGTCTTATGTTATGTTAGTGT 1162
DB 361 TATGCTGAACAACATCGCGCTCTATGTTACAGCTTTCTTGGTCTTATGTTATGTTAGTGT 420
QY 1163 ATTATTCGGCGTACGCTATGTGAACAAGTTTGCTCTCANTTTTCTTGGCCTGTGTCTATGT 1222
DB 421 ATTATTCGGCGTACGCTATGTGAACAAGTTTGCTCTCANTTTTCTTGGCCTGTGTCTATGT 480
QY 1223 GTCCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTTTGTGCTCCACACTTCCC 1282
DB 481 GTCCATCTTGGCTATCTATGCTGGTGCATCAAGTCTTCTTGTCTCCACCACTTCCC 540
QY 1283 GGTCTGCATGCTGGGTAAACCGCACTTTTTCATCAAGACACATTTGCTTGTCTTAAGAC 1342
DB 541 GGTCTGTATGCTGGGCAACCGTACCTGTCTATCAAGACACCTTTGATTTGTCTTAAGAC 600
QY 1343 CAAGGAAATTAACAATGACAGCTCCCATCAAAAGTTTATGGGATTTCTTGTAACTCCGAG 1402
DB 601 CAAGGAGTTTGACAAATGACAGTACATCAAAAGTTTATGGGATTTCTTGTAACTCCGAG 560
QY 1403 TCAATTTTCAATGCCACCTGTGATGAATCTTTGTTTCAATPAACGTCACCTTCAATCC 1461
DB 661 TCAGTTCTTTAATGCCACCTGTGATGAGTACTTTGTTTCAANNTAGCTATCTCAATCC 719

RESULT 13
BE780202 911 bp mRNA linear EST 20-OCT-2000
LOCUS 601468080F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871363 5',
DEFINITION mRNA sequence.
ACCESSION BE780202
VERSION BE780202.1 GI:10201400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 911)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9623 row: p column: 20
High quality sequence stop: 658.
Location/Qualifiers
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/mol_type="mRNA"
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/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

FEATURES
source

BASE COUNT 296 a 205 c 183 g 227 t
ORIGIN

Query Match 13.7%; Score 584; DB 10; Length 911;
Best Local Similarity 94.7%; Pred. No. 1.1e-79;
Matches 714; Conservative 0; Mismatches 25; Indels 15; Gaps 10;

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DB 480 CAGCATTAAGATGACATCTCAGAAAGTCAATGTTTCACTGTTGACACTGTGAGGATAACAA 539

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 16:48:06 ; Search time 1027 Seconds
(without alignments)
11197.279 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4257	99.9	4260	22	AAS59394 Human cDNA encodin
2	4139.4	97.2	4215	22	AAS59388 Human cDNA encodin
3	3152.8	74.0	3367	22	ABA09035 Human K/Cl cotrans
4	2958.8	69.5	6120	22	AAS59390 Mouse cDNA encodin
5	2862.6	67.2	6075	22	AAS59389 Mouse cDNA encodin
6	2732.2	64.1	6052	22	AAS59391 Mouse cDNA encodin
7	1674	39.3	3726	24	ABK63760 Rat sequence diffe
8	1648.4	38.7	3722	25	ACA56531 Human signalling p

9	1584	37.2	3768	24	ABK93499	Human cDNA differe
10	1418	33.3	5239	22	AAS59387	Human cDNA encodin
11	1417.8	33.3	5263	22	AAK51667	Human polynucleoti
12	1416.2	33.2	5261	22	ABA09195	Human K/Cl cotrans
13	1415	33.2	5155	22	AAS59393	Mouse cDNA encodin
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18	1078.8	25.3	2166	22	AAH99377	Human protein enco
19	735	17.3	807	22	AAS59488	Human KCC3 genomic
20	613.4	14.4	2290	22	AAS59490	Frog cDNA encoding
21	530.4	12.5	1941	23	AAK51800	DNA encoding novel
22	514.4	12.1	2384	17	AAT34369	Plasmid pML5 (ATCC
23	514.4	12.1	2384	20	AAZ32244	Human glioblastoma
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25	497	11.7	687	25	ABZ83089	Toxicologically re
26	495	11.6	2420	23	ABL17625	Drosophila melanog
27	434	10.2	489	22	AAS59462	Human KCC3a genom
28	397.2	9.3	2384	12	AAQ14633	Clone associated w
29	343	8.1	416	22	AAI89439	Human polynucleoti
30	335.2	7.9	1713	23	AAS91801	DNA encoding novel
31	262	6.2	1014	22	AAS59396	Mouse potassium-ch
32	253.4	5.9	771	24	ABK34547	Human cDNA for nov
33	245.8	5.8	402	22	AAS59470	Human KCC3 genomic
34	226	5.3	227	25	ACA55696	Human signalling p
35	221.8	5.2	363	22	AAS59471	Human KCC3 genomic
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37	201.4	4.7	323	22	AAS59482	Human KCC3 genomic
38	195	4.6	423	25	ABX36581	Bovine EST associa
39	188.8	4.4	1698	23	AAS91798	DNA encoding novel
40	188.4	4.4	335	22	AAS59486	Human KCC3 genomic
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45	167.6	3.9	291	22	AAS59472	Human KCC3 genomic

ALIGNMENTS

RESULT 1
AAS59394
ID AAS59394 standard; cDNA; 4260 BP.

XX AAS59394;

AC AAS59394;

XX 16-JAN-2002 (first entry)

DT Human cDNA encoding potassium-chloride cotransporter KCC3a.

DE Human; ss: potassium-chloride cotransporter; epilepsy; hypertension;

KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;

KW gene therapy.

XX Homo sapiens.

OS WO200179525-A2.

PN 25-OCT-2001.

PD 16-APR-2001; 2001WO-US12395.

PR 14-APR-2000; 2000US-197350P.

XX (UYVA-) UNIV VANDERBILT.

PA (GAMB/) GAMBA G.

PI Gamba G, Mount DB, Delpire E, George AL;

XX WPI; 2001-611726/70.

DR P-PSDB; AAU39099.

XX New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -
XX
PS Claim 10; Page 291-298; 352pp; English.
XX
CC The invention relates to an isolated and purified, biologically active
CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
CC are used to produce an antibody against KCC, which can be used to detect
CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
CC to screen for candidate substances that can modulate the activity of KCC.
CC KCC and the nucleic acid encoding it can be used to modulate potassium-
CC chloride cotransport in a vertebrate. Therapeutic compositions
CC comprising modulators of the activity of KCC (preferably antibodies or
CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
CC anaemia, and hypertension (also via gene therapy using the KCC
CC polynucleotide). The present sequence encodes a KCC of the invention.
XX
SQ Sequence 4260 BP; 1165 A; 974 C; 972 G; 1146 T; 3 other;

Query Match 99.9%; Score 4257; DB 22; Length 4260;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3841 GCTCAAGTCTTTCAAGCCACTGCTGAGCAGTCAAGGCAAAATTTAGAAATTAACAGCTGA 3900
QY 3901 GCCAATAAATGAATTTGTTAAAGGATGCTAGAAATTTCAACTGAAGAAAAGCAAGTGC 3960
DB 3901 GCCAATAAATGAATTTGTTAAAGGATGCTAGAAATTTCAACTGAAGAAAAGCAAGTGC 3960
QY 3961 AAGTACGTATTTAGCAATTAAGAGATGAATCTCAGAAAGTCAATGTTTCAATGTTGACACTGTG 4020

Db 3961 AAGTACGTATTGAGCAATTAAGATGAATCTCAGAAAGTCATGGTTCATGTTGACACTGTG 4020
Qy 4021 AGGATAACAACCTAGAGAGAGCTTCATCTTACTAAAGAAATTTATGTCGAAGTATATTTGGA 4080
Db 4021 AGGATAACAACCTAGAGAGAGCTTCATCTTACTAAAGAAATTTATGTCGAAGTATATTTGGA 4080
Qy 4081 CCTATTATCTCGGCAAGCCAAAGATGCAAAACATTTTTTTAGCTATATTTCTTTAGTATACC 4140
Db 4081 CCTATTATCTCGGCAAGCCAAAGATGCAAAACATTTTTTTAGCTATATTTCTTTAGTATACC 4140
Qy 4141 CACTGCTGTAATTTTATATTAGGATACCTAACTTTGAAACATGCTGAGCCTCTACTTCTT 4200
Db 4141 CACTGCTGTAATTTTATATTAGGATACCTAACTTTGAAACATGCTGAGCCTCTACTTCTT 4200
Qy 4201 CAAAACATCCCCCAAAATACAGATTTAAATATCCAAAAAATAAAAAAATAAAAAA 4260
Db 4201 CAAAACATCCCCCAAAATACAGATTTAAATATCCAAAAAATAAAAAAATAAAAAA 4260

RESULT 2
AAS59388
ID AAS59388 standard; cDNA; 4215 BP.
XX
AC AAS59388;
XX
16-JAN-2002 (first entry)
XX
DE Human cDNA encoding KCC3a lacking exon 2.
XX
KW Human; ss; potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200179525-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US12395.
XX
PR 14-APR-2000; 2000US-197350P.
XX
PA (UYVA-) UNIV VANDERBILT.
PA (GAMB/) GAMBA G.
XX
PI Gamba G, Mount DB, Delpire E, George AL;
XX
DR WPI; 2001-611726/70.
DR P-PSDB; AAU39093.
XX
PT New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -
XX
PS Claim 10; Page 217-224; 352pp; English.
XX
CC The invention relates to an isolated and purified, biologically active
CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
CC are used to produce an antibody against KCC, which can be used to detect
CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
CC to screen for candidate substances that can modulate the activity of KCC.
CC KCC and the nucleic acid encoding it can be used to modulate potassium-
CC chloride cotransport in a vertebrate. Therapeutic compositions
CC comprising modulators of the activity of KCC (preferably antibodies or
CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
CC anaemia, and hypertension (also via gene therapy using the KCC
CC polynucleotide). The present sequence encodes a KCC of the invention.
XX
SQ Sequence 4215 BP; 1150 A; 961 C; 962 G; 1139 T; 3 other;

Query Match 97.2%; Score 4139.4; DB 22; Length 4215;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 4208; Conservative 0; Mismatches 5; Indels 47; Gaps 2;
Qy 1 TGATAGAGATTTCTTAGTTGGGCTTTTGTGTGGTGAATCAAGGTTATTGAAATG 60
Db 1 TGATAGAGATTTCTTAGTTGGGCTTTTGTGTGGTGAATCAAGGTTATTGAAATG 60
Qy 61 TGTATTATTTTCAAGTTATCTTTTGTATTGTCAGTCAAAAGTAGCTAGCTTAAGAGGAAGAT 120
Db 61 TGTATTATTTTCAAGTTATCTTTTGTATTGTCAGTCAAAAGTAGCTAGCTTAAGAGGAAGAT 120
Qy 121 TTTGCGAGGTTCCCGCCCATCTTTTGTCTTAAAGAGAAACAAAATGATCCTCCAGAAA 180
Db 121 TTTGCGAGGTTCCCGCCCATCTTTTGTCTTAAAGAGAAACAAAATGATCCTCCAGAAA 180
Qy 181 CCACACCAAGATGGCTTCAGTTCGGTTCATGTTGACACCCGACCAAGATCGATGATTC 240
Db 181 CCACACCAAGATGGCTTCAGTTCGGTTCATGTTGACACCCGACCAAGATCGATGATTC 240
Qy 241 CAGGTTTGTGACACACAGTCGCGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA 300
Db 241 CAGGTTTGTGACACACAGTCGCGACNTCAGCTCTCGATCTAGTTCCTCCGAGTAAGATTTA 300
Qy 301 GCTCCCGGAAAGCGTGCCTGAAACAAGCCGAGTGAGCCTATGATGATGAGATGCTGGGG 360
Db 301 GCTCCCGGAAAGCGTGCCTGAAACAAGCCGAGTGAGCCTATGATGATGAGATGCTGGGG 360
Qy 361 CCACACCTTCCTGCGCAACTGTTGCACTGATGACCCAGTGACCGGACTTCTCAACCCC 420
Db 361 CCACACCTTCCTGCGCAACTGTTGCACTGATGACCCAGTGACCGGACTTCTCAACCCC 420
Qy 421 AGGATGTCATCGAGGACCTGAGTCAGACTCCATCACAGGGGAACACAGGCCAACTGTTAG 480
Db 421 AGGATGTCATCGAG- - - - -G 435
Qy 481 ACGACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAATTTATGAAGAGGAG 540
Db 436 ACGACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTTCCAATTTATGAAGAGGAG 495
Qy 541 ATGAATATTTGATAAAAAATTTGGCACTCTTTGAGGAAGAAATGACACACGACCGAAGG 600
Db 496 ATGAATATTTGATAAAAAATTTGGCACTCTTTGAGGAAGAAATGACACACGACCGAAGG 555
Qy 601 TGTCTTCCCTCCTCAACCGCATGGCCAATTTACACTTAATCTGACTCAAGGAGCAAGGAAC 660
Db 556 TGTCTTCCCTCCTCAACCGCATGGCCAATTTACACTTAATCTGACTCAAGGAGCAAGGAAC 615
Qy 661 ATGAAGAGCGCAGAAAAACATCACTGAAGGGAAAAAGAACCCCAAGACCCCAATGG 720
Db 616 ATGAAGAGCGCAGAAAAACATCACTGAAGGGAAAAAGAACCCCAAGACCCCAATGG 675
Qy 721 GTACCTTCATGGGTGCTACCTCCCATGCTTACAAAAATATTTTGGAGTGATCCTTTTTT 780
Db 676 GTACCTTCATGGGTGCTACCTCCCATGCTTACAAAAATATTTTGGAGTGATCCTTTTTT 735
Qy 781 TACGCTTTACATGGGTGGTGGGCACAGCTGGAGTTCTTCAGGCTTTTGCATTTGCTTTA 840
Db 736 TACGCTTTACATGGGTGGTGGGCACAGCTGGAGTTCTTCAGGCTTTTGCATTTGCTTTA 795
Qy 841 TCTGCTGCTGTGTAACAATGTTGACTGCTATCTCCATGAGTGCCATTTGCCACTAATGGAG 900
Db 796 TCTGCTGCTGTGTAACAATGTTGACTGCTATCTCCATGAGTGCCATTTGCCACTAATGGAG 855
Qy 901 TGGTCCAGCTGGGGGCTCATACTTTATGATTTCCCGGGCACTGGGCCAGAGTTGGTG 960
Db 856 TGGTCCAGCTGGGGGCTCATACTTTATGATTTCCCGGGCACTGGGCCAGAGTTGGTG 915
Qy 961 GGGCTGTTGGCCTCTGCTTTTATCTTGGTACCACATTTGACGACGACCTGATCATCTTG 1020
Db 916 GGGCTGTTGGCCTCTGCTTTTATCTTGGTACCACATTTGACGACGACCTGATCATCTTG 975

Qy	1021	GTGCCATTGAAATCTTTCTGTGCTATATATCGTGTCCCGAGCTGCCATCTTTTCACAGTGATG	1081
Db	976	GTGCCATTGAAATCTTTCTGTGCTATATATCGTGTCCCGAGCTGCCATCTTTTCACAGTGATG	1035
Qy	1081	ACGCACTCAAGGAATCAGCAGCCATGCTAAATACATACGCGTGTCTACGGCACAGCTTTCT	1140
Db	1036	ACGCACTCAAGGAATCAGCAGCCATGCTAAATACATACGCGTGTCTACGGCACAGCTTTCT	1095
Qy	1141	TGGTCCTTATGGTATTAGTGGTATTTATCGCGGTACGCTATGTGAACAAGTTTGGCTCAN	1200
Db	1096	TGGTCCTTATGGTATTAGTGGTATTTATCGCGGTACGCTATGTGAACAAGTTTGGCTCAC	1155
Qy	1201	TTTTCTCGCCCTGTGTCAATGTGTCCATCTTTGGCCATCTATGCTGGAGCCATCAAGTCTT	1260
Db	1156	TTTTCTGGCCCTGTGTCAATGTGTCCATCTTTGGCCATCTATGCTGGAGCCATCAAGTCTT	1215
Qy	1261	CTTTTGTCTCTCCACACTTCCCGGTCTGCATCTGGGTAAACCGCACCTTTTCATCAAGAC	1320
Db	1216	CTTTTGTCTCTCCACACTTCCCGGTCTGCATCTGGGTAAACCGCACCTTTTCATCAAGAC	1275
Qy	1321	ACATTGACGTTTGTCTTAAGACCAAGGAAATTTAAACAACATGACAGTCCCATCAAAGTTAT	1380
Db	1276	ACATTGACGTTTGTCTTAAGACCAAGGAAATTTAAACAACATGACAGTCCCATCAAAGTTAT	1335
Qy	1381	GGGAGTCTTCTGTAACTCGAGTCAATTTTTCAATGCCACTGTGTGATGAATACTTTGTTTC	1440
Db	1336	GGGAGTCTTCTGTAACTCGAGTCAATTTTTCAATGCCACTGTGTGATGAATACTTTGTTTC	1395
Qy	1441	ACAATAAGTCACITCAATCCAGGGCACTCTCGATTGGCTAGTGGTATTAATTACAGAGA	1500
Db	1396	ACAATAAGTCACITCAATCCAGGGCACTCTCGATTGGCTAGTGGTATTAATTACAGAGA	1455
Qy	1501	ATCTTTGGAGTAAATTACTCCCAAGGGAGAGATCATCGAAAAGCCCTTCAGGCCAAATCTT	1560
Db	1456	ATCTTTGGAGTAAATTACTCCCAAGGGAGAGATCATCGAAAAGCCCTTCAGGCCAAATCTT	1515
Qy	1561	CTGATGCTTAGGCAGCTTAAACCAATGAATATGTTCTTGTGTGACATCACACCTCTCTCA	1620
Db	1516	CTGATGCTTAGGCAGCTTAAACCAATGAATATGTTCTTGTGTGACATCACACCTCTCTCA	1575
Qy	1621	CGCTTCTGTTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGGCTGGATCAACAGAT	1680
Db	1576	CGNTTCTGTTGGGAATCTTCTTCCCTCTGTTACAGGTATCATGGCTGGATCAACAGAT	1635
Qy	1681	CTGGAGATCTGAAGAGTGCTCAGAAGTCTATTCCGATTGGTACTATCTTTGCCATCTCTGA	1740
Db	1636	CTGGAGATCTGAAGAGTGCTCAGAAGTCTATTCCGATTGGTACTATCTTTGCCATCTCTGA	1695
Qy	1741	CCACCTCTTTGTTTATTTAAGCAATGTTCTTTTGGTGCATGATTTGAAGGGGTTG	1800
Db	1696	CCACCTCTTTGTTTATTTAAGCAATGTTCTTTTGGTGCATGATTTGAAGGGGTTG	1755
Qy	1801	TTCTCAGAGCAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGTAGGCACCTTATCTT	1860
Db	1756	TTCTCAGAGCAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGTAGGCACCTTATCTT	1815
Qy	1861	GGCCATCCCATGGGTGATTGTTATTGGCTCTCTTTTCAACATGTGGGGCTGGACTTC	1920
Db	1816	GGCCATCCCATGGGTGATTGTTATTGGCTCTCTTTTCAACATGTGGGGCTGGACTTC	1875
Qy	1921	AGAGCCTCAGAGTGCAACGAGGCTGTACAAGCTATTGCGAAGGTAAACATCATACCGT	1980
Db	1876	AGAGCCTCAGAGTGCAACGAGGCTGTACAAGCTATTGCGAAGGTAAACATCATACCGT	1935
Qy	1981	TTCTGAGGGTTTTTGGCCACAGCAAGCCAAATGGGNAACCTACTCTGGGCTTTTACTTTAA	2040
Db	1936	TTCTGAGGGTTTTTGGCCACAGCAAGCCAAATGGGNAACCTACTCTGGGCTTTTACTTTAA	1995
Qy	2041	CTGCTGCATTGACAGCCTTGGAAATCTCAATGCTCCCTGGATCTTTGTGGCCCCCAATTC	2100
Db	1996	CTGCTGCATTGACAGCCTTGGAAATCTCAATGCTCCCTGGATCTTTGTGGCCCCCAATTC	2055
Qy	2101	TTTTCCATGTTTTTTCTCATGTGTTTACCTCTTTGTGTAACCTTGGCATGTGCTTCGAAACAT	2160

Db 3136 TATCAAAAACAGAGCGAGACAGAGAGGCCAAATTGGTGAAGACCCGAACTCAATGCTTAC 3195
Qy 3241 GATTGACCAAGCTTGGCTCTGATGAGGACGAAGAGACAGAAACCTTATCAGGAGAAAGTGC 3300
Db 3196 GATTGACCAAGCTTGGCTCTGATGAGGACGAAGAGACAGAAACCTTATCAGGAGAAAGTGC 3255
Qy 3301 ACATGACTTTGGACAAAGCAAAAGTACATGGCATCCCGGGGACAAAGGCAAGTCAATGG 3360
Db 3256 ACATGACTTTGGACAAAGCAAAAGTACATGGCATCCCGGGGACAAAGGCAAGTCAATGG 3315
Qy 3361 AAGGATTCAGGACCTGCTTAACATGCTGTCGGACAGTCCAAATGTGAGGCGGATGCATA 3420
Db 3316 AAGGATTCAGGACCTGCTTAACATGCTGTCGGACAGTCCAAATGTGAGGCGGATGCATA 3375
Qy 3421 CAGCAGTGAACCTCAACGAGGTTATAGTTAAAGTCCCATGAAGCAAGAGCTGTTTAT 3480
Db 3376 CAGCAGTGAANNTCAACGAGGTTATAGTTAAAGTCCCATGAAGCAAGAGCTGTTTAT 3435
Qy 3481 TGAATATGCCAGGGCCACCCCGAAACCCCTGAGGGTGATGAAACCTACATGGAGTTCCTAG 3540
Db 3436 TGAATATGCCAGGGCCACCCCGAAACCCCTGAGGGTGATGAAACCTACATGGAGTTCCTAG 3495
Qy 3541 AGGTGCTTACCGAGGACCTAGAGCGAGTCTTACTTGTCCGGGTGGTGCAGTGAAGTGA 3600
Db 3496 AGGTGCTTACCGAGGACCTAGAGCGAGTCTTACTTGTCCGGGTGGTGGCAGTGAAGTGA 3555
Qy 3601 TCACCATTTTATCATAACTTACTCTGAATGACCGTGTGACCTGTTTCTTTAAAGGCC 3660
Db 3556 TCACCATTTTATCATAACTTACTCTGAATGACCGTGTGACCTGTTTCTTTAAAGGCC 3615
Qy 3661 TAGTCTCTCCATGGAAGTCCAGCTCATTTACTACCCTCCCACTCAACTAGAGGCTGTG 3720
Db 3616 TAGTCTCTCCATGGAAGTCCAGCTCATTTACTACCCTCCCACTCAACTAGAGGCTGTG 3675
Qy 3721 TTCTGTACATCATACTGAACTCTTTGATGAGCTGAGCCTCAAGTACCTGTGTAAAGAG 3780
Db 3676 TTCTGTACATCATACTGAACTCTTTGATGAGCTGAGCCTCAAGTACCTGTGTAAAGAG 3735
Qy 3781 CTCCCATCTGATCTGAGTCATTTACAGAAAGCAAAATATTCCTCAACATCAGAACAT 3840
Db 3736 CTCCCATCTGATCTGAGTCATTTACAGAAAGCAAAATATTCCTCAACATCAGAACAT 3795
Qy 3841 GCTCAAGTCTTTCAAGCCACTGTCTGAGCAGTCAAAAGGCAAAATTTAGAAATTAACAAGCTGA 3900
Db 3796 GCTCAAGTCTTTCAAGCCACTGTCTGAGCAGTCAAAAGGCAAAATTTAGAAATTAACAAGCTGA 3855
Qy 3901 GCCAATAAATGAATTTGGTAAAGGGATGCTAGAAATTTCAACTGAAGAAAAAAGCAAGTC 3960
Db 3856 GCCAATAAATGAATTTGGTAAAGGGATGCTAGAAATTTCAACTGAAGAAAAAAGCAAGTC 3915
Qy 3961 AAGTACGTATTCAGCAATTAAGATGAATCTCAGAGCTCATGTTCAATGTTGACACTGTG 4020
Db 3916 AAGTACGTATTCAGCAATTAAGATGAATCTCAGAGCTCATGTTCAATGTTGACACTGTG 3975
Qy 4021 AGGATAACAACCTAGACAGCTTCATCTTACTAAAGAAATTTATGGTCAAGTATATTGGA 4080
Db 3976 AGGATA - CACTAGACAGCTTCATCTTACTAAAGAAATTTATGGTCAAGTATATTGGA 4033
Qy 4081 CCTATTATCTCGGCAAGCAAGATGCAACATTTTTTTAGCTATATTTCTTTAGTATACC 4140
Db 4034 CCTATTATCTCGGCAAGCAAGATGCAACATTTTTTTAGCTATATTTCTTTAGTATACC 4093
Qy 4141 CACTGCTGAATTTTATATTAGGATACCTACTTGAACATGGCTGCGAGCTCTACTTCTT 4200
Db 4094 CACTGCTGAATTTTATATTAGGATACCTACTTGAACATGGCTGCGAGCTCTACTTCTT 4153
Qy 4201 CAAAAACATCCCCCAAAATACCAGATTTTAAATATCCAAAAAATAAAAAAATAAAAAA 4260
Db 4154 CAAAAACATCCCCCAAAATACCAGATTTTAAATATCCAAAAAATAAAAAAATAAAAAA 4213

ID ABA09035 standard; cDNA; 3367 BP.
XX AC ABA09035;
XX DT 11-JAN-2002 (first entry)
XX DE Human K/Cl cotransporter homologue-encoding cDNA, SEQ ID NO:811.
XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; actin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.
XX OS Homo sapiens.
XX WO200157188-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US03800.
XX 03-FEB-2001; 2000US-0496914.
PR 27-FEB-2000; 2000US-0560875.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI: 2001-457740/49.
XX P-PSDB; ABB11791.
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX Claim 1; Page 717-718; 1963pp; English.
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis; cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g. osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness.
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX

SQ Sequence 3367 BP; 889 A; 775 C; 811 G; 892 T; 0 other;

Query Match 74.0%; Score 3152.8; DB 22; Length 3367;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3176; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy	435	GACCTGAGTCAGAACTCCATCACAGGGGAACACAGCCAACTGTTAGACGAGGACATAAG	494
Db	186	GACCTGAGTCAGAACTCCATCACAGGGGAACACAGCCAACTGTTAGACGAGGACATAAG	245
Qy	495	AAAGCTCGAAATGCTTATCTCAATAATTCCTCAATTAATGAAGAGGAGATGAATATTTGAT	554
Db	246	AAAGCTCGAAATGCTTATCTCAATAATTCCTCAATTAATGAAGAGGAGATGAATATTTGAT	305
Qy	555	AAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTGTCTTCCCTCCTC	614
Db	306	AAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTGTCTTCCCTCCTC	365
Qy	615	AACCCGATGGCCAAATACACTAATCTGACTCAAGGAGCAAGGAAACATCAAGAGGACGAA	674
Db	366	AACCCGATGGCCAAATACACTAATCTGACTCAAGGAGCAAGGAAACATCAAGAGGACGAA	425
Qy	675	AACATCACTGAAGGGAAGAAAGCCACCAAGACCCCAAAATGGGTACCTTCATGGGT	734
Db	426	AACATCACTGAAGGGAAGAAAGCCACCAAGACCCCAAAATGGGTACCTTCATGGGT	485
Qy	735	GTCTACCTCCCATGCTCAAAATATTTTGGAGTGATCCTTTTATACGCTTACATGG	794
Db	486	GTCTACCTCCCATGCTCAAAATATTTTGGAGTGATCCTTTTATACGCTTACATGG	545
Qy	795	GTGGTGGGCACAGCTGGAGTCTTCAGAGCTTTTGAATTTGCTTATCTGCTGCTGCT	854
Db	546	GTGGTGGGCACAGCTGGAGTCTTCAGAGCTTTTGAATTTGCTTATCTGCTGCTGCT	605
Qy	855	ACAATGTTGACTGCTATCTCCATGAGTGCATTTGAGTGATCCTTTTATACGCTTACATGG	914
Db	606	ACAATGTTGACTGCTATCTCCATGAGTGCATTTGAGTGATCCTTTTATACGCTTACATGG	665
Qy	915	GGCTCATATTTATGATTTCCGGGACCTGGGCCCAGAGTTTGGTGGGGCTGTGGCCCTC	974
Db	666	GGCTCATATTTATGATTTCCGGGACCTGGGCCCAGAGTTTGGTGGGGCTGTGGCCCTC	725
Qy	975	TGCTTTTATCTGGTACCACTTTGACGAGGACATGATACCTTTGGTGCCATTCGAATC	1034
Db	726	TGCTTTTATCTGGTACCACTTTGACGAGGACATGATACCTTTGGTGCCATTCGAATC	785
Qy	1035	TTTCTGGTCTATATCGTCCCGAGCTGCCATCTTTTCAAGTATGACGACTCAAGGAA	1094
Db	786	TTTCTGGTCTATATCGTCCCGAGCTGCCATCTTTTCAAGTATGACGACTCAAGGAA	845
Qy	1095	TCAGCAGCATGCTAAATAACATGGGTGTCTACGACACAGCTTTTCTGGTCCCTTATGGTA	1154
Db	846	TCAGCAGCATGCTAAATAACATGGGTGTCTACGACACAGCTTTTCTGGTCCCTTATGGTA	905
Qy	1155	TTAGTGGTATTTATCGGCTAGCTATGTGAACAAGTTTGCCTCANTTTCTGCGCTGT	1214
Db	906	TTAGTGGTATTTATCGGCTAGCTATGTGAACAAGTTTGCCTCANTTTCTGCGCTGT	965
Qy	1215	GTCAATGTTGCTCCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTTGTCTCCTCCA	1274
Db	966	GTCAATGTTGCTCCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTTGTCTCCTCCA	1025

Qy	1275	CACCTCCGGTCTGCATGCTGGGTAAACCGGACTCTTTTCATCAAGACACATTCAGCTTTGC	1334
Db	1026	CACCTCCGGTCTGCATGCTGGGTAAACCGGACTCTTTTCATCAAGACACATTCAGCTTTGC	1085
Qy	1335	TCTAAGACCAAGGAAATTAACAAATGACAGTCCCATCAAAAGTTATGGGATTTCTTCTGT	1394
Db	1086	TCTAAGACCAAGGAAATTAACAAATGACAGTCCCATCAAAAGTTATGGGATTTCTTCTGT	1145
Qy	1395	AACCTCGAGTCAATTTTTCATGCGCACTGTGATGAATATCTTTGTTCAAAATACCTCACT	1454
Db	1146	AACCTCGAGTCAATTTTTCATGCGCACTGTGATGAATATCTTTGTTCAAAATACCTCACT	1205
Qy	1455	TCAATCCAGGCACTTCTGGATTTGGCTAGTGGTATTAATACAGAGAACTTTTGGAGTAAT	1514
Db	1206	TCAATCCAGGCACTTCTGGATTTGGCTAGTGGTATTAATACAGAGAACTTTTGGAGTAAT	1265
Qy	1515	TACCTACCAAGGAGAGATCATCGAAAGCCTTCAGCCAAATCTTCTGATGTCTTAGGC	1574
Db	1266	TACCTACCAAGGAGAGATCATCGAAAGCCTTCAGCCAAATCTTCTGATGTCTTAGGC	1325
Qy	1575	AGCTTAAACCATGAATATGTTTGTGACATCACCACTCTCTCACGCTTCTGGTGGGA	1634
Db	1326	AGCTTAAACCATGAATATGTTTGTGACATCACCACTCTCTCACGCTTCTGGTGGGA	1385
Qy	1635	ATCTTCTTCCCTCTGTGTACAGGTATCATGCTGGATCAAAACAGATCTGGAGATCTGAAA	1694
Db	1386	ATCTTCTTCCCTCTGTGTACAGGTATCATGCTGGATCAAAACAGATCTGGAGATCTGAAA	1445
Qy	1695	GATGCTCAGAAGTCTATTTCGATTTGGTACTATCTTGGCATCTTGACCACTCTTCTGT	1754
Db	1446	GATGCTCAGAAGTCTATTTCGATTTGGTACTATCTTGGCATCTTGACCACTCTTCTGT	1505
Qy	1755	TATTTAAAGCAATGTTGCTCTTTTGTGATGATTAATGAAGGGTGTGTTCTCAGAGACAAG	1814
Db	1506	TATTTAAAGCAATGTTGCTCTTTTGTGATGATTAATGAAGGGTGTGTTCTCAGAGACAAG	1565
Qy	1815	TTCCGTGATGCTGAAAGGTAAATTTGGTGTAGGACCTTATCTTGGCCATCCCCATGG	1874
Db	1566	TTCCGTGATGCTGAAAGGTAAATTTGGTGTAGGACCTTATCTTGGCCATCCCCATGG	1625
Qy	1875	GTGATGTTATTTGGCTCTCTTTTCAACATGTGGGCTGGACTTCAGAGCTTCACAGGT	1934
Db	1626	GTGATGTTATTTGGCTCTCTTTTCAACATGTGGGCTGGACTTCAGAGCTTCACAGGT	1685
Qy	1935	GCACGAGGCTGTCAAGCTATTGCCAAGGATTAACATCAPACGTTTCTGAGGGTTTTT	1994
Db	1686	GCACGAGGCTGTCAAGCTATTGCCAAGGATTAACATCAPACGTTTCTGAGGGTTTTT	1745
Qy	1995	GGCCACAGCAAGCCAAATGGGGAACCTTACCTGGGCTTTACTTTAACTGTGCCATTCGA	2054
Db	1746	GGCCACAGCAAGCCAAATGGGGAACCTTACCTGGGCTTTACTTTAACTGTGCCATTCGA	1805
Qy	2055	GAGCTTGGAAATACATCTTCTGATCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT	2114
Db	1806	GAGCTTGGAAATACATCTTCTGATCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTT	1865
Qy	2115	CTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGGCAACATTAATTCGAACACCC	2174
Db	1866	CTCATGTTTACCTCTTTGTAAACTTGGCATGTGCTTGGCAACATTAATTCGAACACCC	1925
Qy	2175	AACCTGGAGACCCCGATCCCGCTACTACATTTGGGCTTCTTTTCATGGGAATGAGTATC	2234
Db	1926	AACCTGGAGACCCCGATCCCGCTACTACATTTGGGCTTCTTTTCATGGGAATGAGTATC	1985
Qy	2235	TGCTGCTGCTGTGATGTTTCTTCTGCTGATTTATGCTGCTGATTTGCTGCTGATTTAGCT	2294
Db	1986	TGCTGCTGCTGTGATGTTTCTTCTGCTGATTTATGCTGCTGATTTGCTGCTGATTTAGCT	2045
Qy	2295	GGTATGATCTCAAGTACATTTGAATACCAAGGAGCTGAGAAAGAAATGGGTGATGTTATC	2354
Db	2046	GGTATGATCTCAAGTACATTTGAATACCAAGGAGCTGAGAAAGAAATGGGTGATGTTATC	2105
Qy	2355	CGTGGGCTGCTCCTCAGTCAGCGCCGGTTTGTCTTGTGCTTGTGATTTGGAGAGGACCTCCA	2414

QY 162 AAAATGTCATCTCCAGAAACCAACCAAGATGGCTTCAGTTTCGGTTCATGGTGACACCG 221
DB 1 AAAATGTCATCTCCAGAAACCAACCAAGATGGCTTCAGTTTCGGTTCATGGTGACACCA 60
QY 222 ACAAGATCGATGACATTCAGGTTTGTGACAGACCAAGTCCGGAGNCTCAGCTCTCGATCT 281
DB 61 ACTAAGATTGATGACATTCAGGTTTGTGACAGACCAAGCCCGGACNCTCAGCTCTCGGTC 120
QY 282 AGTTCCCGAGTAAGATTAGCTCCCGGAAAGCGTCCGTGAACCAAGCCGGAGTGAGCT 341
DB 121 AGTTCTCGAGTAAGATTAGCTCCCGGAAAGCGTCCGTGAACCAAGCCGTAGTGAGCT 180
QY 342 ATGAGTGAGATCTCTGGGSCCAACCACTTCGCTGGCAACTGTGTGCACTGTGATCCACCCAGT 401
DB 181 ATGACGGAACCTCTCTGGGCTACTACTCTCTGGCAACTGTGTGCACTGTGATCCCTCCAGT 240
QY 402 GACCGGACTTCTCACCCCGAGGATGTCATCGAGGACCTGAGTCAGAACTCCATCACAGGG 461
DB 241 GACCGGACTTCTTAATCCCCAGGATGTTAGCGGAGGACCCCGAGTCAGAACTCCATCACAGGG 300
QY 462 GNAACAGGCAACTGTTAGACGACGCACTAAGAAAGCTCGAAATGCTTATCTCAATAAT 521
DB 301 GAGCACGACGCTGTTAGATGACGCGCCATAAAGGCGGAAATGCTTATCTCAATAAT 360
QY 522 TCCAAATTATGAAGAGGAGATGAATAATTTGATNAAAATTTGGCACTCTTTGAGGAAGAA 581
DB 361 TCCAACTATGAAGAGGAGAGCAATATTTGATNAAAATTTGGCACTCTTTGAGGAAGAA 420
QY 582 ATGGACACGACCAAGGATGTTCTCCCTCCTCAACCGCATGGCCAAATTAACAATAATCTG 641
DB 421 ATGGACACGACCAAGGATGTTCTCTCTCAACCGCATGGCCAAATTAACAATAATCTG 480
QY 642 ACTAAGAGGCAAGGAAATGAAGAGGCAAGAAATCATCACTGAAGGAAAGAAAGAGCC 701
DB 481 ACACAAGAGGCAAGGAAATGAAGAGGCAAGAAATCATCACTGAAGGAAAGAAAGAGCT 540
QY 702 ACCAAGACCCCAATGGTACCTTTCATGGTGCTACCTCCCATGCTTACAAATATT 761
DB 541 ACCAAGACCCCAATGGTACTTTTCATGGTGCTACCTCCCATGCTTACAAATATT 600
QY 762 TTTGAGTGATCTCTTTTATACGCTTACATGGGTGGTGAGGACAGCTGGAGTTCTTCAG 821
DB 601 TTTGAGTGATCT 660
QY 822 GCTTTTGAATGCTCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
DB 661 GCTTTTGAATGCT 720
QY 882 GCCATGCGCACTAATGGAGTGGTCCAGCTGGGGCTCATCTTTATGATTTCCCGGCA 941
DB 721 GCCATGCGCACTAATGGAGTGGTCCAGCTGGGGCTCATCTTTCATGATTTCCAGAGCC 780
QY 942 CTGGGCCCAGAGTTTGGTGGGCTGTGGGCTCTGCTTTTATCTTTGGTACACATTTGCA 1001
DB 781 CTGGGCCCAGAGTTTGGCGGGCTGTAGGCTCTGCTTTTATCTTTGGCACCAATTTGCA 840
QY 1002 GCAGCCATGTATCTCTTGGTGCCATTTGAATCTTTCTGGTCTATATGCTCCCGGAGCT 1061
DB 841 GCAGCCATGTATCTCTTGGTGCCATTTGAATCTTTCTGGTCTATATGCTCCCGGAGCT 900
QY 1062 GCCATCTTTCAGAGTATGACGCACTCAAGGATCAGGAGCATGCTAAATACATGCGT 1121
DB 901 GCCATCTTTCAGAGTATGACGATGCANTCAAGGAGTCAAGGAGTATGCTGAACCAATGCGC 960
QY 1122 GTCTACGCGCAGAGCTTCTTGGTCTCTTATGATGATTTAGTGATTTATTCGGGCTAGCTAT 1181
DB 961 GTCTATGGTACAGGCTTCTTGGTCTCTTATGATGATTTAGTGATTTATTCGGGCTAGCTAT 1020
QY 1182 GTGAACAAGTTTGGCTCANTTTTCTGGCCCTGTGTCAATTTGTGCTCATCTTGGCCATCTAT 1241
DB 1021 GTGAATAAGTTTGGCTCACTCTTCTGGCCCTGTGTGAATTTGTGCTCATCTTGGCTATCTAT 1080
QY 1242 GCTGAGGCCATCAAGTCTTCTTTTGTCTCTCCACACTTCCCGGCTGTCATGCTGGGTAAC 1301

DB 1081 GCTGTGTCATCAAGTCTTCTTTGCTCCACACACTTCCCGGCTGTATGCTGGGCAAC 1140
QY 1302 CGCACTCTTTTCATCAAGACACATTCAGCTTTGCTCTAAGACCAAGGAAATTAACAACATG 1361
DB 1141 CGTACCCCTGTCTCATCAAGACACCTTGACATTTGCTCTAAGACCAAGGAGTTGACAACATG 1200
QY 1362 ACAGTCCCATCAAAAGTTATGGGATCTTCTGTGTAATCTCGAGTCAATTTTTCAATGCCACC 1421
DB 1201 ACAGTACCATCAAAAGTTATGGGATCTTCTGCAACTCGAGTCACTTTTAAATGCCACC 1260
QY 1422 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1481
DB 1261 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1482 AGTGGTATAATTAACAGAGAACTTTTGGAGTAAATTAACCTACCCCAAGGAGAGATCATCGAA 1541
DB 1321 AGTGGTATAATTAACAGAGAACTTTTGGAGTAAATTAATTAACCAAGGAGAGATTAATGAA 1380
QY 1542 AAGCCTTCAGCCAAATCTTCTGATGCTTGAAGAGCTTTAAACCATGAATATGTTCTTGT 1601
DB 1381 AAGCCATCAGCCAAAGTCTGATGCTTTAGGCAACTTAACCATGAATATGTTCTTGTCT 1440
QY 1602 GACATCACCACTCTTTCAGCTTCTGCTGGTGGGAATCTTCTTCCCTCTGTTACAGGTATC 1661
DB 1441 GATATCACCACTCTTTCAGCTTCTGCTGGTGGGATCTTCTTCTTCCCTCAGAGGTATC 1500
QY 1662 ATGCTGGATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAAAGTCTATTTCCGATGCT 1721
DB 1501 ATGCTGGATCAAAACAGATCTGGAGATCTGAAAGATGCTGAAAGATGCTATTTCCCATGGG 1560
QY 1722 ACTATCTTGGCATCTCTGACCACTCTTGTGTTTATTAAGCAATGTTGCTCTTTTGGT 1781
DB 1561 ACCATCTTGGCATCTCTGACCACTCTTGTGTTTATTAAGCAATGTTGCTCTTTTGGT 1620
QY 1782 GCATGATGGAAGGCTTGTCTCAGAGACAAAGTTCGCTGATGCTGCTGAAAGTAAATTTG 1841
DB 1621 GCATGATGGAAGGAGTGTCTCAGAGACAAATTTGGGATGCTGTTAAAGGGAATTTG 1680
QY 1842 GTGCTAGGCACTTATCTTGGCCATCCCATGGGATGTTGTTTATTTGGCTCTCTTTTCA 1901
DB 1681 GTGCTAGGCACTTATCTTGGCCATCCCGTGGGATGCTGTTATTTGGCTCTCTTTTCA 1740
QY 1902 ACATGTGGGCTGCACTTCAGAGCTTCAGAGCTTCAGAGCTTCAGAGCTTCAGAGCTATGCT 1961
DB 1741 ACATGTGGGCTGGCTGCAGAGCTTCAGAGCTTCAGAGCTTCAGAGCTTCAGAGCTATGCT 1800
QY 1962 AAGGATAACTATACCGTTCTGAGGCTTTTGGCCACAGCAAGCAATGGGGAACCT 2021
DB 1801 AAGGATAACTATACCTTCTTGGGATTTTGGTTCAGCAAGCAATTAATGGGGAACCT 1860
QY 2022 ACCTGGCTTTTATCTTAACTGCTGCAATTCAGAGCTTGGAACTATTCATTTCCCTGCT 2081
DB 1861 ACCTGGCTTTTATCTTAACTGCTGCAATTCAGAGCTTGGAACTATTCATTCGCTCTGCT 1920
QY 2082 GATCTGTGGCCCCCAATCTTTTCCATGTTTTTCTCATGTTTACCTCTTTTGAACCTG 2141
DB 1921 GATCTGTGGCCCCCAATCTTTTCCATGTTTTTCTCATGTTTACCTCTTTTGAACCTG 1980
QY 2142 GCATGCTCTTGCNAACATTTCTTCGAACACCCAACTGGAGACCCCGATTCGCTACTAC 2201
DB 1981 GCTTGTGCTTGCNAACATTTCTTCGAACACCCCACTGGAGGCTTCGATTCGCTATAT 2040
QY 2202 CATTTGGGCTCTTCTTTCATGGGAATGAGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 2261
DB 2041 CATTTGGGCTCTTCTTTCATGGGAATGAGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
QY 2262 TGGTATTTATGCCATTTGAGCCATGGTAAATAGCTGGTATGATCTACAAGTACATTTGAATAC 2321
DB 2101 TGGTATTTATGCCATTTGAGCTATGGTAAATAGCTGGCATGATCTACAAGTACATTTGAATAT 2160
QY 2322 CAAGGAGCTGAGAAAGATGGGATGGTATGCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCT 2381

2161	Db	CAAGGGGCTGAGAAAGAAATGGGGGATGGTATCCGTGGGGCTGTCGCTCAGTCAGCGAGCCCGC	22220
2382	Qy	TTTGTCTTTGCTTCGATTTGGAGGAAGACCTCCACACACTAAAACTGGAGGCCTCAGTTG	2441
2221	Db	TTTGGCTTTGCTTCGCTTAGAGGAAGGACCTCTCTCACACTAAAACTGGAGGCCTCAGCTG	2280
2442	Qy	CTTGTATTACTGAAACTTAGATGAGAGACTTATCATGTCAAGCATCTCGCTCTCTCACTTT	2501
2281	Db	CTCGTCTCTAGAGCTGGATGAAGATTTACAGCTCAAGCACCGCTCGCTCTCTCAGCTTT	2340
2502	Qy	GCCTCAGAGCTCAAGCAGGAAAAAGGTTTCACTATTGTGGGGCTCTGTCATCGTGGGGGAAC	2561
2341	Db	GCCTCCAGGCTCAAGCAGGAAAAAGGACTCACGATTTGTGGGCTCTGTCTATCGTGGGGGAAC	2400
2562	Qy	TTTCTAGAGAACTACGGTGAAGCTTTTAGCTGTCTGAGCAGACCAATAAGCACCTTAATGGAG	2621
2401	Db	TTCTTTGAGAACTATTGTGTGACGGCTCGCGCAGAGCAGACCAATTAAGCACCTTAATGGAG	2460
2622	Qy	GCAGAGAAGGTAAAAAGGATTTCTGCCAGCTGGTGGTGGCCGCCAAGCTGAGAGAGGGCAATT	2681
2461	Db	GCAGAAAGGTAAAAAGGATTTCTGCCAATTGGTGGTGGCTGCCAAGCTGAAGAGGGCAATT	2520
2682	Qy	TCCCACTCATCCAGTCATGTGGCCTTGGGGGCAATGAAGCACAAACGCTGGTGTGATGGGC	2741
2521	Db	TCACACCTCATCCAGTCTCTGTGGCNTCGAGGCAATGAACAACAACAGTGGTGTGATGGGC	2580
2742	Qy	TGGCCTTAATGGCTGGGCTCAAAAGCAAGATGCCCGCGCTTTGGAGAGACTTTTATTGGCACA	2801
2581	Db	TGGCCCAATGGCTGGGCTCAGAGTGAAGATGTCTCGCGCTTTGGAAAGACTTTTCAATTGGCACA	2640
2802	Qy	GTTCCGAGTGAACAATGCTGTGCCCATCTTTGCACTGCTGGTGGCTAAAAACATCTCCTCTTTT	2861
2641	Db	GTAAGAGTGAACAATGCTGTGCCCATCTAGCCCTGCTGGTGGCTAAAAATGCTCCTCTTTT	2700
2862	Qy	CCCAGCAATGTGGAGCAAAATTTTCTGAGGGCAAACTGATGTGTGGTGGATTTGTCATGAT	2921
2701	Db	CCCAGCAATGTGGAGCAAGTTTCTGAGGGCAAACTGATGTGTGGTGGATTTGTCATGAT	2760
2922	Qy	GGGGGGATGCTTATGCTACTACCAATTCCTACTGAAACAGCACAGAGTGTGCGCAAGTGC	2981
2761	Db	GGGGGCATGCTCATGCTATTACCGGTTCTGTGCTGAAACAGCACAGGTTTGGCGGAAATGC	2820
2982	Qy	AGCATACGGATCTTTCACAGTAGCCCCAATTAGAAGACAAACAGTATCCAAATGAAGAAGGAC	3041
2821	Db	AGCATACGGATCTTTCACAGTAGCCCCAATAGAAGACAAACAGTATCCAGATGAAGAAGAT	2880
3042	Qy	CTAGCCACTTTCCTATATCATCTTACGATTTGAGCGGAGGTAGAAGTGGTGGAGATGCAT	3101
2881	Db	CTGGCCACTTTCCTGTATACCACTCGCATTTGAGCGAAGTTGGAAGTGGTGGAGATGCAC	2940
3102	Qy	GACAGTGATATATCAGCATATACTTTACGAGCGCACTTTGATGTGGAACAAAGTCCCGAG	3161
2941	Db	GACAGTGACATATCTGGCCTATACATATGAGCGCACCTGTATGATGAGAGCAGAGTCCCGAG	3000
3162	Qy	ATGCTTTCGGCAGATCGCGCTATCCAAACAGAGCGGAGACAGAGAGGCACAATTTGGTCAAA	3221
3001	Db	ATGCTTTCGGCAGATCGCGCTATCCAAACAGAGCGGAGACAGAGAGGCACAAGTGGTCAAA	3060
3222	Qy	GACCGAAACTCAATGCTACGATTGACCAAGCAATTTGGCTCTGATGAGGACGAAGAGACAGAA	3281
3061	Db	GATCGAAACTCAATGCTACGTTGACCAAGCAATTTGGCTCTGATGAGGACGAAGAGACAGAA	3120
3282	Qy	ACCTATCAGGAGAGGTGCCATGACTTTGGCAAAAGACAGTACATGGCATTCCCGGGGA	3341
3121	Db	ACGTACCAAGGAGAGGTGCCATGACTTTGGCAACCAAGGATAAATACATGGCATTCCCGGGGG	3180
3342	Qy	CAAAAAGCGAAAGTCAATGGAAGGATTTCCAGGACCTGCTTAACTATGCGTCCGAGCAGTCC	3401
3181	Db	CAAAAAGTCAAGTCAATGGAAGGATTTCCAGGACCTCTTAATATGCGTCCGAGCAGTCC	3240
3402	Qy	AATGTGAGCGGAGTGCATACAGCAGTGAACCTCAACGAGGTTATAGTTAACTAGTCCCAT	3461
3241	Db	AACGTGAGACGGAGTGCATACAGCAGTGAAGCTCAATGAAGTTATAGTCAACCAAGTCTCAT	3300

Qy	3462	GAAGCAAGCTGTTTATTTGAATATATGCCAGGCGCACCCCGAAACCCCTGAGGGTGATGAA	3521
Db	3301	GAAGCAAGCTGTTTATTTGAATATATGCCAGGACCAACCCCGGAACCCCTGAAGGTGATGAA	3360
Qy	3522	AACTACATGAGATTCCTAGAGGTGCTTACCGAGGACTAGAGCGAGTCCCTACTTGTGTCGG	3581
Db	3361	AACTACATGGAATTTCTAGAAGTGTCTACCTGAGGGATTTAGAACGAGTCTCTTGTGTCGG	3420
Qy	3582	GGTGGTGGCAGTGAAGTGATCACCAATTTATTTATAACCTACTCTGTAATGACCGTGCTTGA	3641
Db	3421	GGTGGTGGCAGTGAAGTTCATCACCAATTTACTCATATACGCTGTGGGAGATTTCTGCGTGG	3480
Qy	3642	CTGTGTTTTTTAAAAGGCCTAGCTCTCCATGGAAGTGCAGCTCATATTACCACTCCC	3701
Db	3481	TCCGACTTCCCTAA--GACTCATCGTCCATGAGGATGATAGCTCTTCTTCCTACCACTCCC	3537
Qy	3702	ACTCAACTAGNAGCCTGTGTTCTGTACACATCATCTGTAACCTCTTGATGAGCTGAGGCTC	3761
Db	3538	ACTC-----TATTTCTGCAGAGCTGAGGCCCC	3563
Qy	3762	AAGTACCTGTGTAAGAAGCTCCCATCTGTATCTGCAGTCAATTACAGAAAAAGCAAAATATT	3821
Db	3564	ATCTATGCTCTT-----GGCTGCAACATGATCTGC--CATCCAGCAGCAAAACAAATAAT	3615
Qy	3822	CCCTCAACATCAGAACAAATGCTCAAGTCTTTCGAAGCCACTGTCTGAGCAGCTCAAAAGCAA	3881
Db	3616	CCCTCAA--CAGAAAGAAATGGTCAAGTCTTAAAGCTATTCTTATGCGACGAGAAAGGCAA	3672
Qy	3882	ATTAGAATTTAACAGCTGAGCCAA-----TAAATGAATTTGG	3917
Db	3673	GTCAAAATTTAACAGCTTAAAGCCAAAGGGAACCTTTTGGCCACACAGAAGGTAATGAGTTAG	3732
Qy	3918	TAAAGGGATGCTAGAAATTTCAACTGAAGAAAAAAAAGCAAGTCAAGGTACGTTATTTCAGCAT	3977
Db	3733	TAAAACATATGCTAGAAATGTAACTGTGCCAACAGAACCA---ATGTTTCATATCTCAACAT	3788
Qy	3978	TAAAGATGAATCTCAGAAGTCATGGTTCAATGTTGAC	4014
Db	3789	TCAGGACGAGTTTTCAGAAGACACGGGTCAGTGAGCAC	3825

RESULT 5

IP AAS59389 standard: cDNA: 6075 BP.

XX AAS59389;

XX
DT 16-JAN-2002 (first entry)

XX DE Mouse cdNA encoding KCC3a lacking exon 2.

XX	
KW	Mouse; ss; potassium-chloride cotransporter; epilepsy; hypertension;
KW	KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW	gene therapy.

AA
OS
Mus sp..

AA PN WO200179525-A2.

XX PD 25-OCT-2001.

XX
PF 16-APR-2001: 2001WO-US12395.

XX
PR 14-APR-2000: 2000US-197350P.

XX (UYVA-) UNIV VANDERBILT.

XX
PA (GAMB/) GAMB G.

PI Gamba G, Mount DB, Delpire E, George AL;

WPI; 2001-611726/70.

DR P-PSDB; AAU39094.

Qy	1962	AAGGATAACATCATACCGTTTCTGAGGGTTTTGGCCACAGCAAGCCAAATGGGGAACCT	2021
Db	1756	AAGGATAACATCATACCTTTCTTAGGGTTTTTGGTCACAGCAAGCTAATGGGAACCT	1815
Qy	2022	ACCTGGGCTTTACTTCTAACTGCTGCCAATTCGACAGAGCTTGGAAATACTCATTTGCCCTCCCTG	2081
Db	1816	ACCTGGGCTTTACTTCTAACTGCTGCCATAGCAGAGCTGGGAATTCATCATCGCTCCCTG	1875
Qy	2082	GATCTTGTGGCCCCAAATCTTTCCATGTTTTTTCTCATGTGTAACTCTTTGTAAACTTG	2141
Db	1876	GAICTCTGGCCCCAATNTTTCATGTTTTTCTCATGTGTAACTCTTTGTGAACCTG	1935
Qy	2142	GCATGTCCCTTGC AAAACATTACTTTCGAAACCCCAACTGGAGACCCCGAATCCGCTACTAC	2201
Db	1936	GCTTGTCCCTTGC AAAACATTACTTTCGAAACCCCAACTGGAGGCTCGAATCCGCTAATAT	1995
Qy	2202	CATTGGGCCCTTTCTTTTCATGGGAATCAGTATCTGTCTGGCTCTGATGTTTCATTTCTTCC	2261
Db	1996	CATCTGGGCCCTTCTTTTCATGGGAATCAGTATCTGTCTGGCTCTGATGTTTCATTTCTTCT	2055
Qy	2262	TGTTATTATGCCAATTTAGCCATCGTAAATAGCTGGTATGATCTACAAGTACATTGAATAC	2321
Db	2056	TGTTATTATGCCAATTTAGCTATGTTAATAGCTGGCATGATCTACAAGTACATTGAATAT	2115
Qy	2322	CAAGGAGCTGAGAAAGAAATGGGTGATGTTATTCGTGGGCTGTCCCTCAGTCAGAGCCCGG	2381
Db	2116	CAAGGGCTGAGAAAGAAATGGGGGATGGTATCCGTGGGCTGTCCCTCAGTCAGAGCCCGC	2175
Qy	2382	TTTGTCTTTGCTTCGATTTGGAGGAGGACCTCCACACACTAAAACTGGAGGCTCAGTTG	2441
Db	2176	TTTGTCTTTGCTTCGCTAGAGGAAGGACCTCTCACACTAAAACTGGAGGCTCAGCTG	2235
Qy	2442	CTTGTATTACTGAAACTAGATGAAGACTTACATGCTCAAGCATCCTCGCCTCTCCACCTTT	2501
Db	2236	CTCGTCTCTACTGAAGCTGGATGAAGATTTACACGTCAAGCACCTCGCCTCTCCACCTTT	2295
Qy	2502	GCCTCAGAGCTCAAAGCAGGAAAAGTTNCACTATTGTGGGCTCTGTCATCGTGGGGAAC	2561
Db	2296	GCCTCCAGAGCTCAAAGCAGGAAAAGGAGCTCACGATTTGTGGGCTCTGTCATCGTGGGGAAC	2355
Qy	2562	TTCTCTAGAGAACTACGCTGAAGCTTTTAGCTGTGAGCAGACCAATAAAGCACCTTAATGGAG	2621
Db	2356	TTCTTGGAGAACTATGTGTACGCGCTCGCGCAGACAGACCAATTAAGCACCTTAATGGAG	2415
Qy	2622	GCAGAGAGGTAAAAGGATTTGCCAGCTGGTGGTGGCCGCAAGCTGAGAGAGGCAATT	2681
Db	2416	GCAGAAAAGGTAAAAGGATTTGTCGCAATTTGTGGTGGCTGCAAGCTGAAAGAGGCAATT	2475
Qy	2682	TCCACACTCATCCAGTCATGTGGGCTTTGGGGGCAATGAAGCACACACGCTGGTGTATGGGC	2741
Db	2476	TCACACCTCATCCAGTCTGTGGGCTCGAGAGGCAATGAAAACACACAGTGGTGTATGGGC	2535
Qy	2742	TGGGCTTAATGGCTGGGCTCAAAGCGAAGATGSCCGCGCTTTGGAAGACTTTTATTGGGCACA	2801
Db	2536	TGGGCCAATGGCTGGGCTCAGATGAAGATGCTCGCGCTTGGAAAGACTTTCAATTGGCACA	2595
Qy	2802	GTTTCGAGTGACAACTGCTGGCCACTTTGCACTGCTGTGGCTAAAAACAATCTCCTTCTTT	2861
Db	2596	GTACGAGTGACAACTGCTGGCCACTTAGCCCTGCTGGTGGGCTAAAAAATGTCTCCTCTTT	2655
Qy	2862	CCCAGCAATGTGGAGCAATTTCTGAGGGCAACATTCATGTGTGGTGGATTTGTCATGAT	2921
Db	2656	CCCAGCAATGTGGAGCAAGTTTTCTGAGGGCAACATTCATGTGTGGTGGATTTGTCATGAT	2715
Qy	2922	GGGGGGATGCTTATGCTACTACCAATTCTCTACTGAAAACAGCAACAGGTGTGGCCAAAGTGC	2981
Db	2716	GGGGGCATGCTCATGCTATTACCGTTCTGTCTGAAAACAGCACAGGTTTGGCGGAATGC	2775
Qy	2982	AGCATACGGATCTTTCACAGTAGCCCAATTTAGAAGACAAACAGTATCCAAATGAAGAAGGAC	3041
Db	2776	AGCATACGGATCTTTCACAGTAGCCCAACTAGAAGACAAACAGTATCCAGATGAAGAAGGAT	2835

Qy	3042	CTAGCCACCTTCCTTATATCACTTACGGATTTGAGCGGAGGTAGAAAGTGTGGAGATGTCAT	3101
Db	2836	CTGGCCACCTTTCTGTACCACTCGCGCATTTGAGCGAAGTGAAGTGTGGAGATGTCAC	2895
Qy	3102	GACAGTGATATATCAGCATATACTTACGAGCGACCTTTTGATGATGGAACAAAGTCTCCAG	3161
Db	2896	GACAGTGACATATCTGCCTATACATATGAGCGCACCTTGATGATGGACGAGAGTCTCCAG	2955
Qy	3162	ATGCTTCGGCACATGCGGCTTATCCAAACAGAGCGAGACAGAGAGGACCAATTTGGTGA	3221
Db	2956	ATGCTTCGGCATATGCGGCTGTCCAAACAGAGCGAGACAGAGGACCAAGTGTGAA	3015
Qy	3222	GACCGAACTCAATCTACGATTTGACAGCATTTGGCTCTGATGAGGACGAAGACAGAA	3281
Db	3016	GATCGAAACTCAATGCTACGCTTGACAGCATTTGGCTCTGATGAGGACGAAGACAGAA	3075
Qy	3282	ACCTATCAGGAGAGGTGCACATGACTTGCACAAAGACAAAGTACATGGCATCCCCGGGA	3341
Db	3076	ACGTAACAGGAGAGGTGCACATGACTTGCACCAAGATAAATACATGGCATCCCCGGG	3135
Qy	3342	CAAAAACGGAAGTCAATGGAAGGATTCAGGACCTGCTTAACTATGCGTCCGGACCAAGTCC	3401
Db	3136	CMAAGGTCAGTCAATGGAAGGATTCAGGACCTACTTAAATATGCGTCCGGACCAAGTCC	3195
Qy	3402	AATGTGAGCGGATGCATACAGCAGTGAACTCAACGAGGCTTATAGTTTACAAAGTCCCAT	3461
Db	3196	AACGTGAGACGGATGTCATACAGCAGTGAAGCTCAATGAAGTTATAGTTCACAAAGTCTCAT	3255
Qy	3462	GAACAAAGCTGGTTTTATTGAATATGCCAGGGCCACCCCGAAACCTCGAGGGTGATGAA	3521
Db	3256	GAACAAAGCTGGTTTTGTTGAATATGCCAGGACCCCGGAACCTCGAGGGTGATGAA	3315
Qy	3522	AACATCATGAGATTCTAGAGGTGCTTACCGAGGACATAGAGGAGTCTCTACTTGTCCGG	3581
Db	3316	AACATCATGGAATTTCTAGAAAGTGTCACTGAGGAGATTTAGAACGAGTCTTCTTGTCCGG	3375
Qy	3582	GGTGGTGGCAGTGAAGTGATCACCATTTATTCATAACTACTCTGAATGACCGTGTGTA	3641
Db	3376	GGTGGTGGCAGTGAAGTGATCACCATTTATTCATAACTACTCTGAATGACCGTGTGTA	3435
Qy	3642	CCTGTTTTCTTAAAGGCCTACGTCCTCCATGGAAGTGCCAGCTCATTAACCACTCCC	3701
Db	3436	TCCGACTTCCCTAA---GACTCATCGTCCATGAGATGATAGTCTTTCTCACTCCCTCCC	3492
Qy	3702	ACTCACTAGAACCTGTGTTCTGTACATCATACTGAACTCTTGATGAGCTGAGCGCTC	3761
Db	3493	ACTC-----TATTCTGCGAGCTGAGCGCCC	3518
Qy	3762	AAGTACCTGTGTAAGAGCTCCCATCTGATCTGCAGTCAATACAGAAAAAGCAAAATATT	3821
Db	3519	ATCTATGCTCTT-----GGCTGCACATGATCTGC---CATCCGACGAGAAACAAATTAAT	3570
Qy	3822	CCCTCAACATCAGAACCAATGCTCAAGTCTTTCAAGCCACTGTCTGACGAGTCAAGGCAA	3881
Db	3571	CCCTCAA---CAGAAAGATGCTCAAGTCTTAAAGCTATTCTTATGCGAGAGAGGCAA	3627
Qy	3882	ATTAGAAATTACAGCTGAGCCAA-----TAAATGAATTGG	3917
Db	3628	GTCAAAATTTACAGCTTAAGCCAAAGGGAACCTTTTGGCACACAGAAGGTAAATGAGTTAG	3687
Qy	3918	TAAAGGGATGCTAGAAATTTCAACTGAAGAAAAAAAGCAAGTCAAGTACGTTATTCAGCAT	3977
Db	3688	TAAACATATGCTAGAAATGTACTGGCAACAGAAAGCA---ATGTTTCATATCTCAACAT	3743
Qy	3978	TAAAGATGAATCTCAGAAAGTCATGGTTCAATGTTGAC	4014
Db	3744	TCAGACGAGTTTTCAGAAACACGGGTCAAGTACGAGTAC	3780

RESULT 6
AAS59391
ID AAS59391 standard; cDNA; 6052 BP.
XX

AC AAS59391;
 XX 16-JAN-2002 (first entry)
 XX
 XX Mouse cDNA encoding potassium-chloride cotransporter KCC3b.
 DE
 XX Mouse; ss; potassium-chloride cotransporter; epilepsy; hypertension;
 KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
 KW gene therapy.
 XX
 XX Mus sp..
 OS
 XX WO200179525-A2.
 PN
 XX 25-OCT-2001.
 PD
 XX 16-APR-2001; 2001WO-US12395.
 PF
 XX 14-APR-2000; 2000US-197350P.
 PR
 XX (UYVA-) UNIV VANDERBILT.
 XX (GAMB/) GAMBA G.
 PA
 XX Gamba G, Mount DB, Delpire E, George AL;
 XX
 XX WPI; 2001-611726/70.
 DR P-PSDB; AAU39096.
 DR
 XX New isolated and purified potassium-chloride cotransporter polypeptide
 PT for detecting a modulator of potassium-chloride cotransporter that can
 PT treat epilepsy, sickle cell anaemia, and hypertension -
 XX
 XX Claim 10; Page 254-262; 352pp; English.
 PS
 XX The invention relates to an isolated and purified, biologically active
 CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
 CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
 CC are used to produce an antibody against KCC, which can be used to detect
 CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
 CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
 CC to screen for candidate substances that can modulate the activity of KCC.
 CC KCC and the nucleic acid encoding it can be used to modulate potassium-
 CC chloride cotransport in a vertebrate. Therapeutic compositions
 CC comprising modulators of the activity of KCC (preferably antibodies or
 CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
 CC anaemia, and hypertension (also via gene therapy using the KCC
 CC polynucleotide). The present sequence encodes a KCC of the invention.
 XX
 XX Sequence 6052 BP; 1633 A; 1397 C; 1380 G; 1639 T; 3 other;
 SQ

Query Match 64.1%; Score 2732.2; DB 22; Length 6052;
 Best Local Similarity 86.6%; Pred. No. 0;
 Matches 3120; Conservative 0; Mismatches 408; Indels 76; Gaps 7;
 435 GACCTGAGTCAGAACTCCATCACAGGGGACACAGCCAACTGTTAGACAGCGGACATAG 494
 206 GACCCGAGTCAGAACTCCATCACAGGGGAGCACAGCCAGCTGTTAGATGACGGCCATAA 265
 495 AAAGCTCGAAATGCTTATCTCAATATCCCAATATGAGAGGAGATCAATATTTCGT 554
 266 AAAGCCCGAATGCTTATCTCAATATCCCAATATGAGAGGAGATCAATATTTCGT 325
 555 AAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCCGAAAGGTGTCTCCCTCCTC 614
 326 AAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCCGAAAGGTGTCTCTCTCCTC 385
 615 AACCCGATGGCCAAATACACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGCGAGAA 674
 386 AACCCGATGGCCAAATACACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGCGAGAG 445
 675 AACATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 734
 446 AACATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 505

QY 735 GTCTACCTCCCATGTCCTACAAAATATATTTTGGAGTGATCCTTTTACGCCCTTACATGG 794
 DB 506 GTCTACCTCCCATGTCCTACAAAATATATTTTGGAGTGATCCTTTTACGCCCTTACATGG 565
 QY 795 GTGTGGGACACAGCTGGAGTTCTTCAGGCTTTTGCATTTGCAATTTGCTTATCTGCTGCTGCTGT 854
 DB 566 GTAGTGGGAAACAGCTGGAAATCTTCAGGCCCTTTGCAATTTGCTTATCTGCTGCTGCTGT 625
 QY 855 ACAAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTTAATGGAGTGGTGCCAGCTGGG 914
 DB 626 ACAAATGTTGACTGTCTATCTCCATGAGTGCCATTTGCCACTTAATGGAGTGGTGCCAGCTGGG 685
 QY 915 GGCTCATATCTTTATGATTTCCGGGCACTGGGCCAGAGTTTGGTGGGCTGTGTGGCCCTC 974
 DB 686 GGCTCATATCTTTATGATTTCCAGAGCCCTGGGCCAGAGTTTGGGCGGCTGTAGGCCCTC 745
 QY 975 TGCCTTTATCTTTGGCACCACATTTGCAGAGCCCATGTATATTTCTTTGGTGCCATTTGAAATC 1034
 DB 746 TGCCTTTATCTTTGGCACCACATTTGCAGAGCCCATGTATATTTCTTTGGTGCCATTTGAAATC 805
 QY 1035 TTTCTGGTCTATATCGTCCCGGAGCTGCCATCTTTTCAAGTGATGACGCACTCAAGGAA 1094
 DB 806 TTTCTGGTCTATATCGTCCCGGAGCTGCCATCTTTTCAAGTGATGACGCACTCAAGGAA 865
 QY 1095 TCAGCAGCCATGCTAAATTAACATGCGTGTCTACGSCACAGCTTTCTTGGTCTTATGTTA 1154
 DB 866 TCAGCAGCCATGCTAAATTAACATGCGTGTCTACGSCACAGCTTTCTTGGTCTTATGTTA 925
 QY 1155 TTAGTGGTATTTATCGGGGTAGCTATGTGAACAAGTTTGGCTCANTTTTCTTGGCCCTGT 1214
 DB 926 TTAGTGGTATTTATCGGGGTAGCTATGTGAACAAGTTTGGCTCANTTTTCTTGGCCCTGT 985
 QY 1215 GTCAATGTTGTCATCTTGGCCATCTATGCTGGAGCATCAAGTCTCTTTTGGCTCTCCA 1274
 DB 986 GTCAATGTTGTCATCTTGGCCATCTATGCTGGAGCATCAAGTCTCTTTTGGCTCTCCA 1045
 QY 1275 CACTTCCCGGTCTGATGCTGGGTAACCGCACTCTTTTCAATCAAGACACATTTGACATTTGC 1334
 DB 1046 CACTTCCCGGTCTGATGCTGGGTAACCGCACTCTTTTCAATCAAGACACATTTGACATTTGC 1105
 QY 1335 TCTAAGACCAAGGAATTAACAACATGACAGTCCATCAAGATTTATGGGATTTCTTGT 1394
 DB 1106 TCTAAGACCAAGGAATTTGACAAATGACAGTCCATCAAGATTTATGGGATTTCTTGT 1165
 QY 1395 AACTCGAGTCAATTTTCAATGCTGACATGAATTTTGTTCACAAATACCTCACT 1454
 DB 1166 AACTCGAGTCAATTTTCAATGCTGACATGAATTTTGTTCACAAATACCTCACT 1225
 QY 1455 TCAATCCAGGCAATTCCTGGATTTGGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 1514
 DB 1226 TCAATCCAGGCAATTCCTGGATTTGGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT 1285
 QY 1515 TACCTACCAAGGAGAGATCATCGAAAGCCCTTCAGCAAAATCTTCTGATGCTTTAGGC 1574
 DB 1286 TATTTACCAAGGAGAGATTAATTTGAAAGCCATCAGCAAAATCTTCTGATGCTTTAGGC 1345
 QY 1575 AGCTTAAACCAATGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1634
 DB 1346 AACTTAAACCAATGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1405
 QY 1635 ATCTTCTTCT 1694
 DB 1406 ATCTTCTTCT 1465
 QY 1695 GATGCTCAGAAAGTCTATTTCCGATTTGGTATCTATCTTGGCCATCTTGGCACTCTGAGCACTCTTGT 1754
 DB 1466 GATGCCAGAAAGTCTATTTCCCATTTGGGACCATCTTGGCCATCTTGGCACTCTGAGCACTCTTGT 1525
 QY 1755 TATTTAAGCATGTTGCTCTTTTGGTGCATGTTTGAAGGGTGTGTTCTCAGAGCAAG 1814
 DB 1526 TATTTAAGCATGTTGCTCTTTTGGTGCATGTTTGAAGGGTGTGTTCTCAGAGCAAG 1585

1815 TTGCGTGTGCTGTAAGAGTAAATTTGGTGTAGGACCTTATCTTGGCCATCCCATGG 1874
1816 TTTGGGATGCTGTAAAGGAAATTTGGTGTAGGACCTTATCTTGGCCATCCCATGG 1645
1817 GTGATGTTATTTGGTCTCTTTTCAACATGTGGGCTTGGACTTTCAGAGCCTCAAGGT 1934
1818 GTGATGTTATTTGGTCTCTTTTCAACATGTGGGCTTGGACTTTCAGAGCCTCAAGGT 1705
1935 GCACCGAGCTGCTACAGCTATTTGCCAAGGTAACATCATACCTTTCTTGGAGGTTTTT 1994
1706 GCGCTCGGCTGCTGAGGCTATCGCCAAAGGTAACATCATACCTTTCTTGGAGGTTTTT 1765
1995 GCGCAGCAAGCAAGCAAGCTTACCTCGGCTTTTACTTCTAACTGCTGCCATTGCA 2054
1766 GGTACAGCAAGCAAGCTTACCTCGGCTTTTACTTCTAACTGCTGCCATTGCA 1825
2055 GAGCTTGGAAATCTCAATGCTCTCTGGAATCTTGTGGCCCAATCTTTCCATGTTTTT 2114
1826 GAGCTGGGAAATCTCAATGCTCTCTGGAATCTTGTGGCCCAATCTTTCCATGTTTTT 1885
2115 CTCATGTTTACTCTTTGTAACCTTGGCATGTCTTGCCTTGCACCAATCTTTCGAACCCC 2174
1886 CTCATGTTTACTCTTTGTAACCTTGGCATGTCTTGCCTTGCACCAATCTTTCGAACCCC 1945
2175 AACTGGAGACCCGATTTCCGCTACTACCAATTTGGCCCTTTCTTCAATGGGAATGATATC 2234
1946 AACTGGAGCCCTCGATTTCCGCTATTTACTTGGCCCTCTCTTCAATGGGAATGATATC 2005
2235 TGTCTGGCTCTGATGTTCAATTTCTTCTGCTATTTATGCAATTTGAGCCATGTAATAGCT 2294
2006 TGTCTAGCTCTGATGTTCAATTTCTTCTGCTATTTATGCAATTTGAGCTATGTAATAGCT 2065
2295 GGTATGATCTACAGTACATTAATCAAGGAGCTGAGAAAGATGGGTGATGGTATC 2354
2066 GGCATGATCTACAGTACATTAATCAAGGAGCTGAGAAAGATGGGTGATGGTATC 2125
2355 CGTGGCTCTGCTCAGTCAGCCGCTTGTCTTGTCTGATTTGGAGGAGCACTCCA 2414
2126 CGTGGCTCTGCTCAGTCAGCCGCTTGTCTTGTCTGATTTGGAGGAGCACTCTCT 2185
2415 CACACTAAAACTGGAGGCTCAGTGTCTGATTTACTGAACTAGATGAAGCTTACAT 2474
2186 CACACTAAAACTGGAGGCTCAGTGTCTGATTTACTGAACTAGATGAAGCTTACAC 2245
2475 GTCAAGCATCTCGCTCCTCAGTGTCTGATTTACTGAACTAGATGAAGCTTACAT 2534
2246 GTCAAGCATCTCGCTCCTCAGTGTCTGATTTACTGAACTAGATGAAGCTTACAC 2305
2535 ATTGTGGGCTCTGCTCAGTGTGGGAACTTCTTAGAGAACTACGGTGAAGCTTTAGCTGCT 2594
2306 ATTGTGGGCTCTGCTCAGTGTGGGAACTTCTTAGAGAACTATGTTGACGGCTCGGGCA 2365
2595 GAGCAGACCAATAAGCACCCTAATGGAGGAGGAGGTAAGGATTTCTGCCAGCTGGTG 2654
2366 GAGCAGACCAATAAGCACCCTAATGGAGGAGGAGGTAAGGATTTCTGCCAATTTGGTG 2425
2655 GTGGCCCGCAGCTGAGAGGGCAATTTCCCACTCATCCAGTCATGTGGCTTGGGGGC 2714
2426 GTGGCTGCCAAGCTGAAGAGGGCAATTTCAACCTCATCCAGTCTGTGGCTCGGAGG 2485
2715 ATGAAGCACAACAGCTGTGATGGGCTGGCTTAATGGCTGGGCTCAAGCGAAGATGCG 2774
2486 ATGAACACACACAGTGTGATGGGCTGGCCCAATGGCTGGGCTCAGAGTGAAGATGCT 2545
2775 CGCGCTTGAAGACTTTTATTTGGCAGAGTTCAGTGACAACTGCTGCCCATCTTGCACCTG 2834
2546 CGCGCTTGAAGACTTTTATTTGGCAGAGTTCAGTGACAACTGCTGCCCATCTTGCACCTG 2605
2835 CTGGTGGCTTAAACATCTCTTCTTCCAGCAATGTGGAGCAATTTCTGAGGCAAC 2894
2606 CTGGTGGCTTAAACATCTCTTCTTCCAGCAATGTGGAGCAATTTCTGAGGCAAC 2665
2895 ATTGATGTGTGGTATTTGTCATGATGGGGGATGCTTATGCTACTACCATTTCTACTG 2954

2666 ATTGATGTGTGGTATTTGTCATGATGGGGCATGCTCATGCTATTACCGTTCCTGCTG 2725
2955 AAAAGCAGCAGAGTGTGGCGAAGTGCAGCATACGGATCTTTCACAGTAGCCCAATTAGAA 3014
2726 AAAAGCAGCAGAGTGTGGCGAAGTGCAGCATACGGATCTTTCACAGTAGCCCAATTAGAA 2785
3015 GACAACTAGTATCCAAATGAAGAAGCCTAGCCACCTTCTTATATCACTTACGCATTGAG 3074
2786 GACAACTAGTATCCAAATGAAGAAGTGCAGCATACGGATCTTTCACAGTAGCCCAATTAGAA 2845
3075 GCGAGGTGAGAGTGTGGAGATGCATGACAGTGTATATCAGCATATATCAGTAGCCG 3134
2846 GCAGAGTGTGAGTGTGGAGATGCATGACAGTGTATATCTGCTATATACATATGAGCGC 2905
3135 ACTTTGATGATGGAACAAAGTCTCCAGATGCTTGGGCATATGCGGCTGTCCAAACACAG 3194
2906 ACCCTGATGATGGAACAAAGTCTCCAGATGCTTGGGCATATGCGGCTGTCCAAACACAG 2965
3195 CGAGACAGAGGACCAATTTGTTGAAGACCGAAACTCAATGCTACGATTTGACAGCAATT 3254
2966 CGAGACAGGAGGACCAATTTGTTGAAGATCGAAACTCAATGNTACGCTTGGACAGCAATT 3025
3255 GGCTCTGATGAGGACGAGACAGAACTTATCAGGAGAGGTGCAATGATTTGGACA 3314
3026 GGCTCTGATGAGGACGAGACAGAACTTATCAGGAGAGGTGCAATGATTTGGACC 3085
3315 AAAGCAAGTACATGCGATCCCGGGGCAAAAGCAAGTCAATGGAAGGATTTCCAGGAC 3374
3086 AAGGATAAATACATGCGATCCCGGGGCAAAAGTCAATGGAAGGATTTCCAGGAC 3145
3375 CTGCTTAACATGCGTCCGACCACTCAATGTGAGCGGATGCATACAGCAGTGAACCTC 3434
3146 CTACTTAATATGCGTCCGACCACTCAATGTGAGCGGATGCATACAGCAGTGAACCTC 3205
3435 AACGAGTATATGTTAAACAGTCCCATGAAGCAAAAGTGGTGTGTTTGAATATGCGAGG 3494
3206 AATGAAGTATATGTTAAACAGTCCCATGAAGCAAAAGTGGTGTGTTTGAATATGCGAGG 3265
3495 CCACCCGAAACCTGAGGGTGTGAAACTACATGGAAGTCTTCTAGAGTGTCTTACCGAG 3554
3266 CCACCCGAAACCTGAGGGTGTGAAACTACATGGAAGTCTTCTAGAGTGTCTTACCGAG 3325
3555 GAGCTAGAGCAGTCTCTTCTGCGGGTGTGCGAGTGAAGTGTATCACCATTATTTCA 3614
3326 GGAATGAGCAGTCTCTTCTGCGGGTGTGCGAGTGAAGTGTATCACCATTATTTCA 3385
3615 TAACTACTGTAATGACCGTGTGACCTGTTTCTTAAAGGCGCTAGTCTTCCATGG 3674
3386 TAACTACTGTAATGACCGTGTGACCTGTTTCTTAAAGGCGCTAGTCTTCCATGG 3442
3675 AAGTCCAGCTCATTTACTACCACTCCCACTCACTAGAGGCTGTGTTCTGTACATCA 3734
3443 AGATGATAGCTTTTCTTACCACTCCCACTCCTTAAAGGCGCTAGTCTTCCATGG 3473
3735 TACTGAACCTTGTGAGTGTGAGCTCAAGTACCTGTGTAAGAGCTCCCACTTGTATCT 3794
3474 TATTTCTGAGAGCTGAGCCCACTTATGCTCTT-----GGTGCACATGATCT 3523
3795 GAGTCAATTTACAGAAAAAGCAATATCCCTCAACATCAGAACTAGTCTTCAAGTCTTCA 3854
3524 GC---CATCCAGCAGAAACAAATATCCCTCAA---CAGAAGAAATGTTCAAGTCTTCA 3577
3855 AGCCTACTGCTGAGCAGTCAAGGCAATTTAGAAATTTACAGCTGAGCCAA----- 3905
3578 AGCTATTTCTATGGCAGGAGGAGCAAGTCAAAATTTAAACAGCTAAGCCAAAGGCACT 3637
3906 TAAATGAATTTGGTAAAGGAGTGTAGAAATTTCAACTGAAGAAAA 3950
3638 TTTGGCACACAGAAAGTAAATGATTTAGTAAACATATGCTAGAAATGTAAGTGGCAAC 3697
3951 AAAGCAAGTCAAGTATTCAGCATTTAAAGATGAATCTCAGAGTCAATGTTCAATGT 4010

Db 3698 AAAGCA---ATGTTTATATTAACATTCAGGACGAGTTTCAGAGACACGGGTCACTGA 3753

Qy 4011 TGAC 4014

Db 3754 GCAC 3757

RESULT 7

ABK63760

ID ABK63760 standard; cDNA; 3726 BP.

XX

AC ABK63760;

XX

DT 18-JUN-2002 (first entry)

XX

DE Rat sequence differentially expressed in response to a hepatotoxin #1667.

XX

Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;

KW

differential expression; centrilobular necrosis; steatosis.

XX

OS Rattus norvegicus.

XX

PN WO200210453-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US23872.

XX

PR 31-JUL-2000; 2000US-222040P.

XX

PR 02-NOV-2000; 2000US-244880P.

PR

PR 11-MAY-2001; 2001US-290029P.

PR

PR 15-MAY-2001; 2001US-290645P.

PR

PR 22-MAY-2001; 2001US-292336P.

PR

PR 06-JUN-2001; 2001US-295798P.

PR

PR 13-JUN-2001; 2001US-297457P.

PR

PR 19-JUN-2001; 2001US-298884P.

PR

PR 09-JUL-2001; 2001US-303459P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;

XX

PI WPI; 2002-241625/29.

DR

XX

PT Predicting toxic effects of compounds or the progression of these toxic

PT

PT effects by determining the changes in gene expression in tissues or

PT

PT cells exposed to the toxin and comparing these to gene expression in

PT

PT unexposed tissues or cells -

XX

PS

PS Claim 1; Seq ID No 1667; 239pp; English.

XX

CC The invention relates to methods for predicting toxic effects of

CC

CC compounds or the progression of these toxic effects by determining the

CC

CC global changes in gene expression in tissues or cells exposed to the

CC

CC toxin and comparing these to gene expression in unexposed tissues or

CC

CC cells. Also included are methods of predicting at least one toxic

CC

CC effect of a compound or progression of a toxic effect, preferably the

CC

CC hepatotoxicity of a compound, comprising detecting the level of

CC

CC expression in a tissue or cell sample exposed to the compound of two or

CC

CC tissues or cell exposed to a known toxin. The genes may be used as
CC toxicity markers in drug screening and toxicity assays. The genes and
CC gene expression information may be used as diagnostic markers for the
CC prediction or identification of the physiological state of tissue or cell
CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.

XX

SQ Sequence 3726 BP; 767 A; 1024 C; 1069 G; 866 T; 0 other;

Query Match 39.3%; Score 1674; DB 24; Length 3726;

Best Local Similarity 71.6%; Pred. No. 0;

Matches 2212; Conservative 0; Mismatches 872; Indels 6; Gaps 1;

Qy

536 AGGAGATCAATATTTTGTATATAAATTTGGCACTCTTTGAGGAAGAAATGGACACCAGACC 595

Db

171 AGGAATGACTACTATGACCGAACCTGGCACTGTTTGAGGAGGAGCTGGACATCGGCC 230

Qy

596 GAAGGTGTCTTCCCTCTCAACCGCATGGCCAAATACACTAATCTGACTCAAGGAGCAAA 655

Db

231 AAAGGTATCATCTCTCTGGGCAAGCTTGTGAGCTATACCAACCTCACCAAGGAGCCAA 290

Qy

656 GGAACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715

Db

291 GGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 350

Qy

716 AATGGGTACCTTTCATGGGTGTCTACCTCCCATGTCTACAAATATTTTGGAGTGATCCT 775

Db

351 CATGGGACCTTATGGAGTGATACCTGCCCTGCTGCAGAAATATCTTCGGGGTATCCT 410

Qy

776 TTTTATACGCTTACATGGGTGGTGGGACAGCTGGAGTCTTTCAGGCTTTTGCAATTGT 835

Db

411 CTTCCTCGGCTGACCTGGATGGTGGGACAGCTGGGCTGCTGCAGGCTCTCTCATTTGT 470

Qy

836 CTTTATCTGCTGCTGTACAAATGTTGACTGCTATCTCCATGATGAGTGCATGGCACTAA 895

Db

471 CCTCATCTGTTGCTGTGTACCTCTGCTGACAGCCATCTCCATGATGATGCTGCCACCA 530

Qy

896 TGGAGTGTGCTGAGCTGGGGCTCATATTTTATGATTTCCCGGCACCTGGGCCACAGATT 955

Db

531 TGGTGTGTTCCAGCTGGTGGCTTCTTACTTCATGATTTCCGCTCTTTTGGACACGAATT 590

Qy

956 TGTGGGGCTGTGGCTCTGCTTTTATCTTTGTTACCAATTTGACAGAGCATGTATCAT 1015

Db

591 CGGAGTGTCTGTGGCTTATGCTTCTACCTGGGACACACATTTTCAGCAGCATGTATAT 650

Qy

1016 CTTTGGTGCAATGAAATCTTTCTGGTCTATATCGTCCCGGAGCTGCCATCTTTCACAG 1075

Db

651 CTTAGGAGCCATTGAGATCTTGTGACCTACATTTGCTCCACAGCTGCCATCTTTTACCC 710

Qy

1076 TGATGACGCACTCAAGGAATCAGCAGCCATGCTAAATAACATGCTGTCTACGGCACAGC 1135

Db

711 ATCGGGACACACACATGATCAAGGCCACCTTGAAATAACATGCGGTGTACGGAACCAT 770

Qy

1136 TTTCTGGTCTCTTATGTTATTTAGTGGTATTTATCGGCTAGCTATGTGAACAAGTTTGC 1195

Db

771 TTTCTGCTTCTATGACCTAGTGGTGTGTTGTCGGTGTCAAGTATGTGAACAAGTTTGC 830

Qy

1196 CTCANTTTCTGGCTGTGTCATTTGTGTCATCTTGGCCATCTATGCTGAGGACCATCAA 1255

Db

831 CTCACCTTCTGGCTGTGTCATCTCCATCTCTCCATTTACGTTGGGAGGACATCAA 890

Qy

1256 GTCTTTCTTTGCTCTCCACACTTTCCGGTGTGATGCTGGTAAACGCACTCTTTTCATC 1315

Db

891 GTCCGCTTTTACCTCTCTGTTTTCGGTGTGATGCTGGGCAATAGGACTCTGTCTCG 950

Qy

1316 AAGACATTTGAGCTTTGCTCTTAAGACAAGGAAATTAACAACATGACAGTCCCATCAA 1375

Db

951 GGACCACTTTGACATCTGTGCCAAGACAGTTGTGGTGCACATGACAGATGGGCCACCG 1010

Qy

1376 GTTATGGGATTTCTTGTGTAACTCGAGTCAATTTTCAATGCCACCTGTGTGATGATACTT 1435

Db	1011	GCTGTGGACTTTCTTCTGCCACAGCCCCAACCTTACTGCTGACTCCTGTGACCCCTACTT	1070
Qy	1436	TGTTTCAATAACGTCACTTCAATCCAGGGCAATCTCTGGATTGGCTAGTGGTATAATTAC	1495
Db	1071	CCTGCTCAACATGTGACAGAGATTCTTGCAATACCTGGGAGAGCTGCTGTGCTCCA	1130
Qy	1496	AGAGAACTTTTGGAGTAATTAACCTACCCAGGAGAGATCATCGAAAAGCCTTCAGCCAA	1555
Db	1131	GGAAAACCTGTGGAGTGTCTTACTTGAGAAAGGTGAGGTGTGGAGAGCATGGGCTGCC	1190
Qy	1556	ATCTTCTGATGCTTAGGAGAGCTTAA-----CAATGAATATGTTCTTGTGATCATC	1609
Db	1191	CTCCACAGATACCTTGGCCTGAAGGAGAGCCTGTCCCTGTATGTGGTGGCGACATCGC	1250
Qy	1610	CACCTCTCTCAGCTTCTGGTGGGAATCTTCTCCCTGCTTACAGGTATCATGCTGG	1669
Db	1251	CACATCTTTCACGCTGCTGGTGGGATCTTTTCTCCCTCTGTAAACAGGCATCATGGCTGG	1310
Qy	1670	ATCAAAACAGATCTGGAGATCTGAAAGATGCTCAGAGTCTATTCGGATTGGTACTATCT	1729
Db	1311	CTCAAAACCGTTCCGGGGACCTCCGTGATGCTCAGAAAGTCTATCCCTGTGGGGACCATCT	1370
Qy	1730	TGCGATCTGACACCTCTCTTGTATTTAAGCAATGTTGCTCTTTTGGTGGATGAT	1789
Db	1371	GGCTATTTGTCACCACTTCACTCGTGTACTTCAGCAGTGTGATTTCTTGGGTGCTGCA	1430
Qy	1790	TGAAGGGTGTCTCAGAGACAAAGTTCGGTGTGCTGTGAAGGTAAATTCGTGCTAGG	1849
Db	1431	CGAGGGTGTGGTCTCCGGGACAAAGTACGGTGTGGCTGATGGCTCAGAGAACTCGTGGTAGG	1490
Qy	1850	CACCTTATCTTGGCCATCCCATGGGTGATTTGTTATTTGGCTCCTTCTTTTCAACATGTGG	1909
Db	1491	CACCTTGGCCTGGCCTTCACTTGGTTCATCGTGGTGGCTCTTCTTCTCAACATGTGG	1550
Qy	1910	GGCTGCACTTCAGAGCTCAGAGTGCACCGAGGTGCTACAAGCTATTTGCCAAGATAA	1969
Db	1551	TGCCGGCCTCCAAAGTCTCACTGGGGCGCACGTTTACTGCAAGCCATTTGCCAAGATAA	1610
Qy	1970	CATCATACCGTTTCTGAGGGTTTTGGCCACAGCAAGCAATGGGAACTTACCTGGGC	2029
Db	1611	CATCATCCCTTCTCCGGGTGTTTGGCCACGGAAAGCAATGTGTAGCCAACTGGGC	1670
Qy	2030	TTTACTTCTAATGCTGCAATTCAGAGCTTGGAACTACTCATTTGCCCTCCCTGGATCTGT	2089
Db	1671	CCTCTCTCTGACAGGCTCATCGCTGAGCTGGGCATCTCATCGCTCCCTTGGATGCT	1730
Qy	2090	GGCCCCAATCTTTCATGTTTTTCTCATGTGTTTACCTCTTTGTAACTGGCATGTGC	2149
Db	1731	GGCCCCCATTTCTCCATGTTCTTCTGATGTGTTTACCTCTTTGTAACTTGGCCTGTGC	1790
Qy	2150	CTTGTCAACATTAATTTCGAACCCCACTGGAGACCCCGATTCGGCTACTACCATTTGGC	2209
Db	1791	TGTGCAGACATTTCTGAGGACCCCACTGGGCGCCCGGTTCAAGTACTATCATCTGGGC	1850
Qy	2210	CCTTTCTTTCATGGGAATCAGTATCTGTCTGGCTCTGATGTTTCAATTTCTCTGGTATTA	2269
Db	1851	GTGTCTTCTTCTGGGCATGAGTCTGTGCTGCTCTCATGTGTTGCTCTCTCTGGTACTA	1910
Qy	2270	TGCCATTGTAGCCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACAGAGAGC	2329
Db	1911	CGCCCTTAGTGGCCATGGTCAATCGCAGGCATGATCTACAAGTATCATCGATACCAAGGGC	1970
Qy	2330	TGAGAAAGATGGGGTATGGTATCCGTGGCTGCTCCCTCAGTGCAGCCCGGTTTGTCTTT	2389
Db	1971	TGAGAAAGATGGGGTATGGGATCCGAGCCCTGTCCCTGAGTGGCGCAGATATGCACT	2030
Qy	2390	GCTTCGATTGGAGGAGGACCTCCACACATAAAACTTGGAGCCCTCAGTTGCTGTATT	2449
Db	2031	GCTGAGACTAGAGGAGGGCTCTCTCACAGGAAGTTCGCGCCTCAGCTCCTGGTCT	2090
Qy	2450	ACTGAACCTAGATGAAGACTTACATGTCAAGCATCTCCGCTCTCTCACTTTGGCTCACA	2509
Db	2091	GCTGAAGTTTAGAGGAGATCTTTCATGTGAAGTACCCCTCGGCTCTCACCTTTGGCTCCA	2150
Qy	2510	GCTCAAGCAGGAAAAAGTNTCACTATTGTGGGCTCTGTCTATCTGTGGGAACTTCTCTAGA	2569
Db	2151	ACTTAAAGCTGGGAAAGSCCTGACAACTGTTGGCTCTGTCTCATCAGGCGCAGCTTCTGGA	2210
Qy	2570	GAACTACGGTGAAGTCTTGTCTGACGACAGCATTAAGCACTTAATGGAGGACAGAA	2629
Db	2211	GAGCTATGGGGAAGCCAGGCTGTCTGAGCAGACAATCAAGAACATGATGGAGATTGAGAA	2270
Qy	2630	GGTAAAGGATTTCTGCCAGCTGTGTGGCGCCCAAGCTGAGAGAGGCAATTTCCCACT	2689
Db	2271	AGTAAAGGCTTCTGCCAGGTAGTGGTGGCCAGCAAGGTTCCGAGAGGGCTGGCCCACT	2330
Qy	2690	CATCCAGTCACTGTGGCCTTGGGGCATGAAGCAACAACCGGTGTGTATGGGTGGCCCTAA	2749
Db	2331	CATCCAGTCTTGGCGCTGGGTGGCATGAGACATACTCCGTGTGTCTGGCTGGCCCTA	2390
Qy	2750	TGGTGGCGTCAAAAGCGAAGATGCCCGCTTTGGAAGACTTTTATTTGGCAGATTCGAGT	2809
Db	2391	TGGCTGGCGACAGAGTGAAGACCCACGTCGCTGGAAGACCTTTATTCGACACTGTGCGCTG	2450
Qy	2810	GACAACTGCTGCCCATCTTGCACCTGCTGGCTGCTAAACACATCTCTCTTTCCAGAA	2869
Db	2451	CACCACAGCTGCCCACTGGCCCTGTGTGGTCCAAAGAACATAGCTTTCTACCCCAAGAA	2510
Qy	2870	TGTGAGCAATTTTCTGAGGGCAACATTTGATGTGTGTGGATTGTGCAATGATGGGGGAT	2929
Db	2511	CCACAGGCTTACCTGGAGGGCCACATTTGATGTGTGTGGTATCGTGCATGACGAGGCAT	2570
Qy	2930	GCTTATGCTACTACATTTCTTACTGAAAACAGCAAGGTGTGGGAAAAGTGCAGATACG	2989
Db	2571	GCTGATGCTGCTGCCCTTCTCTGCTGGCCAGCAAGGTTTGGAAAGAGTGGCGATGCG	2630
Qy	2990	GATCTTCACTAGCCCAATTTAGAAAGCAACAGTATCCAAATGAGAGAGGACCTAGCCAC	3049
Db	2631	CATTTTCACTGGCCAGATGGACGCAACAGCATCCAGATGAAAGAGGATCTGGCCAT	2690
Qy	3050	CTTCCATATCACTTTACGCATTTGAGCGGAGGTGAGAGTGTGGAGATGCAATGACATGA	3109
Db	2691	CTTCTCTGTATCACTCTCCGCTGGAAGCTGGAAGTGGAGTGTGTAGATGCAACAGTGA	2750
Qy	3110	TATATCAGCATATTAATACGAGCGCATTTTATGATGAAACAAAGGTCCCAGATGCTTGC	3169
Db	2751	CATCTCGGCTTACACTTACGAGCGGACACTGATGATGGAGCGCGGTCTCAAAATCTGCG	2810
Qy	3170	GCATATCGGCTATCCAAAACAGAGCGAGACAGAGAGGCAATTTGGTGAAGACGAA	3229
Db	2811	ACAGATGAGGCTTGACCAAAACAGAGCGGGATCGAGAGGCCCAAGCTGGTGAAGGACAGGA	2870
Qy	3230	CTCAATGCTACGATTTGACAGCATTTGGCTCTGATGAGGACGAGCAAGAACCTATCA	3289
Db	2871	CTCGGCTCTGAGGCTTAGAGGCTTACTCTCGACGAGGAGGATGATCTGTACAGGCGC	2930
Qy	3290	GGAGAGGTGCATGACTTGGACAAAAGACAAAGTACATGCGATCCCGGGGACAAAAGC	3349
Db	2931	TGACAAGATCCAGATGACATGGACAGAGACAAAGTACATGCTGAACCTCTGGACCCAG	2990
Qy	3350	GAAGTCAATGAAGATTTCCAGGACCTCTTAAATGCTGCGGACCACTCCAATGTGAG	3409
Db	2991	CAATGCCCTGACAACTTCCGGGAGCTGGTGACATTAAGCGGACCACTCCAATGTGCG	3050
Qy	3410	GGGATGATACAGCAGTGAACCTCAACGAGGTTATAGTTAAACAAGTCCCATTGAAGCAAA	3469
Db	3051	GGGTATGACACTGCTGTGGAAGCTCAATGAAGTCAATGTGCACGCTCCCATTGATGCCCG	3110
Qy	3470	GCTGTTTTTATGAATATGCCAGGCGCACCCCGGAAACCTCAGGCTGATGAATACTACAT	3529
Db	3111	CTGTCTCTACTGAACATGCCCGCCCCCTTAAGAACAGTGAAGGTGATGAGAACTACAT	3170
Qy	3530	GGAGTTCCTAGAGTGTCTTACCGAGGACTAGAGCGAGTCTTACTTTGCGGGGTGGTGG	3589
Db	3171	GGATTTCTTGAAGTCTTAACCGAGGGCTTGAACGGGTGTTGTTGGTGGTGGTGGTGG	3230

QY	3590	CAGTGAAGTGCATCACCAATTTATTTCATAACC	3619
Db	3231	CCGGGAAGTCATCACCATTCTATTCTTGAGC	3260
RESULT 8			
ID	ACA56531	standard; cDNA; 3722 BP.	
XX	ACA56531;		
XX	AC		
XX	XX		
DT	06-JUN-2003	(first entry)	
XX	XX		
DE	Human signalling pathway polynucleotide probe SEQ ID NO 1129.		
XX	XX		
KW	Human; probe; ss; array element; Parkinson's disease;		
KW	signalling pathway population; cancer; adenocarcinoma; leukaemia;		
KW	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.		
OS	Homo sapiens.		
XX	XX		
PN	US6500938-B1.		
XX	XX		
PD	31-DEC-2002.		
XX	XX		
PF	30-JAN-1998;	98US-0016434.	
XX	XX		
PR	30-JAN-1998;	98US-0016434.	
XX	XX		
PA	(INCY-) INCYTE GENOMICS INC.		
XX	XX		
PI	Au-Young J, Seilhamer JU;		
XX	XX		
DR	WPI; 2003-352189/33.		
XX	XX		
PT	Combination of polynucleotide probes, useful as array elements in a		
PT	microarray for monitoring the expression of a number of target		
PT	polynucleotides -		
XX	XX		
PS	Claim 1; SEQ ID NO 1129; 65pp; English.		
XX	XX		
CC	The invention relates to a combination which, comprises a number of		
CC	polynucleotide probes comprising a sequence selected from one of the 1490		
CC	sequences mentioned in the specification. The combination is useful as an		
CC	array element in a microarray for monitoring the expression of a number		
CC	of target polynucleotides. The microarray is particularly useful in the		
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.		
CC	The microarray is useful in diagnostics and treatment regimens, drug		
CC	discovery and development, toxicological and carcinogenicity studies,		
CC	forensics and pharmacogenomics. The microarray is also useful for		
CC	monitoring progression of diseases and for developing sophisticated		
CC	profiles for the effects of currently available therapeutic drugs. The		
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs		
CC	and genomic fragments and in research and diagnostic applications. The		
CC	array can detect changes in expression in a large number of genes coding		
CC	for different signaling pathway populations which can be used to diagnose		
CC	various diseases including cancer e.g. adenocarcinoma and leukaemia,		
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease		
CC	and Parkinson's disease. The present sequence represents a polynucleotide		
CC	probe of the invention.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification but was obtained in electronic format directly from USPTO		
CC	at seqdata.uspto.gov/sequence.html?DocID=06500938B1.		
XX	XX		
SQ	Sequence 3722 BP; 712 A; 1088 C; 1126 G; 796 T; 0 other;		
Query Match 38.7%; Score 1648.4; DB 25; Length 3722;			
Best Local Similarity 71.1%; Pred. No. 0;			
Matches 2196; Conservative 0; Mismatches 888; Indels 6; Gaps 1;			
QY	536	AGAGATGAATATTTTGATAAAAATTTGGCATCTTTGAGGAAGAAATGGACACACGACC	595
Db	226	AGAAATTTGACTACTATGACAGAACTCGGCACTGTTTGAGGAAGAGCTGGACATCCGCC	285

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX Homo sapiens.
XX WO200228999-A2.
XX 11-APR-2002.
XX 03-OCT-2001; 2001WO-US30821.
XX PF
XX 03-OCT-2000; 2000US-237189P.
XX PR
XX (GENE-) GENE LOGIC INC.
XX PA
XX Beazer-Barclay Y, Weisman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX Claim 1; SEQ ID No 70; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3768 BP; 711 A; 1099 G; 1131 G; 827 T; 0 other;
XX
XX Query Match 37.2%; Score 1584; DB 24; Length 3768;
XX Best Local Similarity 70.7%; Pred. No. 0;
XX Matches 2122; Conservative 0; Mismatches 872; Indels 6; Gaps 1;
XX 536 AGGAGATGAATATTTTGATAAAATTTGGCACTCTTTGGAGAAATGGACACGAGACC 595

171 AGGAATTGACTATGACAGGAACCTGGCACTGTTTGGAGAGAGCTGGACATCCGCC 230
596 GAAGGTGTCTTCCCTCTCTCAACCCGATGGCCAAATTTACACTAATCTGACTCAAGGAGCAAA 655
231 AAAGTATCTCTCTCTGGGAAAGCTCGTCAGCTACACCAACCTCACCAGGGCGCCAA 290
656 GGAACATGAAGAGGAGAAACATCACTGAAGGAAAGAAAGAACCCACAGACCCCA 715
291 AGAGCATGAGGAGCCGAGAGTGGGGGAGGACCCCGCGAGGGGAGCCGAGGACCCAG 350
716 AATGGTACCTTTCATGGGTGTCTACCTCCCATGCTACAAATATTTTGGAGTGATCCT 775
351 CATGGGACCTCTCATGGGGTGTACCTGCCCTGCTGCAGAAATATCTTTGGGTTATCCT 410
776 TTTTATCGCCTTACATGGGTGGGACAGCTGGAGTCTTTCAGGCTTTTTCAAATGT 835
411 CTTCCTGGGCTGACCTGGATGGTGGGACAGCAGGTGTGTACAGGCCCTCCTCATCGT 470
836 CTTATCTGCTGCTGTGTACAAATGTTGACTGTCTATCTTCATGAGTGCCATTTGCCACTAA 895
471 GCTTATCTGCTGCTGTGTGTACCTGCTGACGGCCATCTCCATGAGTGCATCGCCACCAA 530
896 TGGAGTGGTCCAGCTGGGGCTCATCTTTATGATTTCCGGGACATGGGCCCGAGGTT 955
531 CGGTGTGGTCCAGCTGGGGCTCCTATTTTCATGATCTCTCTGTCACCTGGGGCCAGAAAT 590
956 TGGTGGGGCTGTGGCCCTCTGCTTTTATCTTGGTACCAATTTTGCAGCAGCATGTACAT 1015
591 TGGAGGTGCTGTGGCCCTGTGCTTCTACCTGGGAACAACATTCGACGAGCAGTGTACAT 650
1016 CTTTGGTGGCAATGAATTTTCTGGTGTATATCGTCCCGAGCTGCCATCTTTTCACAG 1075
651 CTTGGGGCCATCAGATCTTGTGACTGCTACCTATTTGCCACACAGCTGCCATTTTTCACC 710
1076 TGATGAGCACTCAAGAAATCAGCAGCATGCTAAATAACATGCTGTCTAGGCGACAGC 1135
711 ATCGGGTGTCTATGACACGCTGAAATGGCAATATGCTGTGTATGGAGCAT 770
1136 TTTCTTGGTCTTATGATGATTTAGTGGTATTTATCGGCTAGCTGTATGAAACAAGTTTGC 1195
771 TTTCTGACCTTCATGACCCCTGGTGGTGTGGGGTCAAGTATGTGAACAATTTGC 830
1196 CTCANTTTTCTGCTGCTGTGTCATTTGTGTCATCTTGGCCATCTATGCTGAGGACATCAA 1255
831 CTGCTCTCTGCTGCTGTGTGATCATCTCCATCTCTCCATCTATGCTGGGGCATAAA 890
1256 GTCTTCTTTGCTCTCCACATCTCCGGTCTGCTGCTGGGTAAACCGCATCTTTTCATC 1315
891 GTCTATATTTGACCTCCCGTGTTCGGGTATGCTGTGGGCAACAGGACCTGTCTCCG 950
1316 AAGACACATTGACGTTTGTCTTAAGACCAAGAAATTAACAACATGACAGTCCCATCAA 1375
951 GGACAGTTTGACATCTGTGCAAGACAGCTGTAGTGGAACATGAGACAGTGGCCACCA 1010
1376 GTTATGGGATTTCTTGTAACTGAGTCAATTTTCAATGCCACCTGTGATGAATACTT 1435
1011 GCTATGGAGTTTCTTCTGCGACAGCCCCAACCTTTACACGACCTCTGTGACCCCTACTT 1070
1436 TGTTCAAAATACGTCACTTCAATCCAGGCAATCTCTGGATTTGGCTAGTGTATTAATAC 1495
1071 CATGCTCAACAAATGTGACCGAGATCCCTGGCATCCCGGGGAGCTGTGTGTGTCTCA 1130
1496 AGAAGTCTTTGGAGTAATTTACCTACCAGGGAGAGATCATCGAAAGCCTTCAGCCAA 1555
1131 GGAAGACCTGTGGAGCCCTTACCTTGGAGAGGGTGTGACATCGTGGAGAGCATGGGTGCC 1190
1556 ATCTTCTGATGTCTTAGGCAGCTTAAA-----CCATGAATATGTTCTTGTGTGACATCAC 1609
1191 CTCGAGATGCCCCGAGCCTGAAGGAGAGCCTGCTCTGTACGTGTGCTGACATCGC 1250
1610 CACCTCTTCAACGCTCTGTGGTGGAAATCTTCTTTTCCCTCTGTTTACAGGATATCATGGTGG 1669

Db 1251 CACATCTTACCGTCTGGTCCGCATCTTCTTCCCTTCTGTAAACAGGCATCATGGCTGG 1310
Qy 1670 ATCAAAACAGATCTGAGATCTCAAGATGCTCAGAACTTATTCGATTTGGTACTATCCT 1729
Db 1311 CTCAAAACCGCTCTGGGACCTTGGTGAACGCCAAGAGTCTATCCCTGTGGGAGCAATCTCT 1370
Qy 1730 TGCCATCTTGACACCTCTCTTGTATTTAATTAAGCAATGTGTCCTTTTGTGGTCAATGAT 1789
Db 1371 GGCCATCATTAACAATCTCCCTCGTGTACTTACGAGTGTGGTCTCTTTGTGGTCCGCTCAT 1430
Qy 1790 TGAAGGGTGTCTTCAGAGACAAGTTCCGTGATGCTGTGAAGGTAATTTGGTGGTAGG 1849
Db 1431 TGAGGGTGTGGTCTCCGGGACAAGTATGGCGATGGTGTCAAGAGAACTTGGTGGTGG 1490
Qy 1850 CACCTTATCTGGCCATCCCATGGGTGATTTATTTGGCTCTCTTTTCAACATGGG 1909
Db 1491 CACACTGGCTGGCTTACCTTGGGTCACTGTCTATCGGCTCTCTTTTCAACGTGG 1550
Qy 1910 GGCTGGACTTACAGGCTCACAGGTGCACCGAGGCTGTCTACAAGCTATTGCCAAGGATAA 1969
Db 1551 CGCTGGCTCCAGAGCTCACAGGGGACCAACGCTATTGCAAGGCCATTGCCAAGGACAA 1610
Qy 1970 CATCATACCGTTCTGAGGGTTTTGGCCACAGCAAGCAATGGGAACTTACCTGGGC 2029
Db 1611 CATCATCCCTCTCTCCGGGTGTTTGGCCACGCGAAGGTGAATGTGTGAACCCACATGGGC 1670
Qy 2030 TTTACTTCTAACTGTCTGCATTTGCAGAGCTTGAATACTCATTTGCTCCCTCGATCTTGT 2089
Db 1671 ACTCTCTGACGGCACTCATCGCGAGCTGGGCACTTCATCGCCTCTCCCTCGAATGGT 1730
Qy 2090 GGCCCCAATTTCTTCATGTTTTTCTCATGTGTACCTCTTTGTAAACTTGGCATGTGC 2149
Db 1731 GGCCCCCATCTTATCCATGTTCTTCTGATGTGCTACCTGTTCTGTAACCTCGCTGTGC 1790
Qy 2150 CTTGCAAAACATTACTTCGAACACCCAACTGGAGACCCCGAATTCGGCTACTACATTTGGGC 2209
Db 1791 GGTGACAGACACTCTGAGGACCCCAACTGGGCGCCCGGTTCAAGTACTATCACTGGGC 1850
Qy 2210 CTTTCTTTTCATGGGAATCAGTATCTGTCTGGCTCTGATGTTCATTTCTCTCTGTTATTA 2269
Db 1851 GCTGTCTCTTCTGGGCATGAGTCTCTGCTTGGCCCTTATGTTGTCTCTCTCTGGTACTA 1910
Qy 2270 TGCCATTGTAGCCATGGTAAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGGAGC 2329
Db 1911 TGCCCTGTGGCATGCTCATCGCGGCATGATCTACAAATATACAGTACCAAGGGGC 1970
Qy 2330 TGAGAAAGAAATGGGTGTATGTTATCCGTGGGTGTCCCTCAGTGCAGCCCGGTTTGTCTTT 2389
Db 1971 TGAGAAAGGATGGGGTGAACGGATCCGAGGCTGTCCCTGAGCGCTGCCCGCTACGCGCT 2030
Qy 2390 GCTTCGATTGGAGGAGGACCTCCACACATAAATCGAGGCTCAGTTCGTTGTATT 2449
Db 2031 GTTCCGGCTGGAGGAGGGGCTCTCTCACCAAGAACTGGCGGCGCAGCTGCTGGTGTCT 2090
Qy 2450 ACTGAAACTAGATGAAGACTTACATGTCAAGCATCTCGCCTCTCACTCTTGGCTTCA 2509
Db 2091 GCTGAAGCTGACAGGACCTTCACTGAAGTACCCCGGCTCTCACTCTCGCTCCCA 2150
Qy 2510 GCTCAAAGCAGGAAAGGTTNCTACTATTTGGGCTCTGTATGTGGGAACTTCCCTAGA 2569
Db 2151 GCTCAAGGCTGGCAAGGGCTGACCATTTGTTGTTCTGTATCCAGGGAGGCTTCTTGA 2210
Qy 2570 GAACTACGGTGAAGCTTTAGCTCTGAGCAGACCATTAAGCACCTAATGAGGCGAGAA 2629
Db 2211 GAGCTATGGCGAGGCTCAGGCCCGGAGCAGACCATCAAGAAATGATGAATTTAGAA 2270
Qy 2630 GGTAAAGGATTTGCGCAGCTGTGGTGGCGCCCAAGCTGAGAGGGCATTTTCCCACT 2689
Db 2271 GGTGAAGGGCTTCTGCCAGTGTGTGGTGGCCACCAAGGTGCGGAGGGGTGCGCCACT 2330
Qy 2690 CATCCAGTATGTGGCTTGGGGGCAATGAAGCAACAACGCTGGTGTATGGCTTGGCTTAA 2749
Db 2331 CATCCAGTCTGTGGCTTGGGAGGCATGCGGCATAACTCCGTGTGTCTGGCTGGCCCTA 2390

Qy 2750 TGGTCTGGCTCAAAAGCGAAGATGCCCGCTTGAAGACTTTTATGSCACAGTTCCGAGT 2809
Db 2391 CGGCTGGCGACAGAGCGAGGAGCCCGCTGCTGCTGAAGACCTTTCATTGACACCGTGGCTG 2450
Qy 2810 GACAACTGCTGCCCATCTTGCACCTGTGGTGGCTTAAAAACATCTCTCTTTTCCAGCAA 2869
Db 2451 CACTACGGCTGCCACCTTGGCCCTGCTGCTGCCCAAGAACATCGCTTCTTACCCAGCAA 2510
Qy 2870 TGTGAGCAATTTTCTGAGGGCAACATTTGATGTGTGGTGGATTTGTCATGATGGGGGAT 2929
Db 2511 CCAGAGGGCTTACCTGAGGGCCACATAGACGTGTGTGGATCTGTGACGATGTGGGAT 2570
Qy 2930 GCTTATGCTACTACCATTTCTTACTGAAACACGACCAAGGTGTGGGAAAGTGCAGCATACG 2989
Db 2571 GCTCATGCTTCTGCCCCTTCTGCTGCGCCAGCATAGGTCTGGAGGAAGTCCGATGCG 2630
Qy 2990 GATCTTCACTAGTCCCAATTTAGAAGACAACAGTATCCAAATGAAGAAGGACCTTAGCCAC 3049
Db 2631 CATCTTCACTAGTGGCCAGATGGATGACAACAGCATCCAGATGAAGAAGGACCTTGGCTGT 2690
Qy 3050 CTTCTATATCACTTACGATTGAGGGGAGGTAGAGTGTGGAGATGCATGACAGTGA 3109
Db 2691 CTTTCTGTACCATCTGTGGCCCTTGTAGGGCGAGTGGAGTGTGGAGATGCAATAACAGTGA 2750
Qy 3110 TATATCAGCATATATCTTACGAGCGCATTTTGTATGATGGAAACAAAGGTCCCAGATGCTTCG 3169
Db 2751 CATCTCTGCATACACCTTACGAGCGGACGCTCATGTGAGGACGCGTCCGAGATGCTGCG 2810
Qy 3170 GCATATGCGGTATTCACAAAACAGAGCGAGACAGAGAGGCAAAATTTGGTGAAGACCGAAA 3229
Db 2811 GCAGATGAGACTGACCAAGACTGAGCGGGAGCGAGAGCCAGCTGGTCAAGGATCGGCA 2870
Qy 3230 CTCATGTCTACGATTGACCGCATTTGCTCTGATGAGGACGAGAGACAGAGAACCTATCA 3289
Db 2871 CTCGCGCTCTGGGTGGAGAGCCTGTACTCGAGCAGGAAGATGAGTCTGCAGTGGGGGC 2930
Qy 3290 GGAGAAGGTGCACATGACTTGGACAAAAGACAAGTACATGTCATCCCGGGGACAAAAGC 3349
Db 2931 TGACAAAGATCAGATGAGCTGGACAGGACCAAGTACATGACTGAGACCTGGACCCACAG 2990
Qy 3350 GAAGTCAATGGAAGATTTCCAGGACCTGCTTAAACATGCGTCCGGACCAAGTCCAATGTGAG 3409
Db 2991 CCATGCCCTGACAAATTTCCGGAGCTGGTGACATTAAGCGGACCAATCCAATGTGCG 3050
Qy 3410 GCGGATGATACAGCAGTGAACCTCAACGAGGTTTATAGTTAACAGTCCCATGAGCAAA 3469
Db 3051 GCGCATGCACACTGCTGTGAAGCTCAATGAAGTCAATGTACGCGCTCCCGAGCGCCG 3110
Qy 3470 GCTGGTTTTTATGTAATATGCCAGGCGCACCCCGAAACCTCAGGGGTGATGAAAACTACAT 3529
Db 3111 CTTGTTCTCTTAAACATGCTTGGCCACCCAGGACAGTGAAGGCGGACGAGAACTGAT 3170

RESULT 10

AAS59387

ID AAS59387 standard; cDNA; 5239 BP.

XX AC AAS59387;

XX DT 16-JAN-2002 (first entry)

XX DE Human cDNA encoding potassium-chloride cotransporter KCC4.

XX KW Human; ss; potassium-chloride cotransporter; epilepsy; hypertension;

XX KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;

XX OS gene therapy.

XX OS Homo sapiens.

XX PN WO200179525-A2.

XX PD 25-OCT-2001.

XX 16-APR-2001; 2001WO-US12395.
XX PF
XX PR 14-APR-2000; 2000US-197350P.
XX (UYVA-) UNIV VANDERBILT.
XX PA (GAMB/) GAMBA G.
XX
XX Gamba G, Mount DB, Delpire E, George AL;
PI WPI; 2001-611726/70.
XX DR P-PSDB; AAU39092.
XX
XX New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -
XX
XX Claim 24; Page 205-213; 352pp; English.
XX
XX The invention relates to an isolated and purified, biologically active
CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
CC are used to produce an antibody against KCC, which can be used to detect
CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
CC to screen for candidate substances that can modulate the activity of KCC.
CC KCC and the nucleic acid encoding it can be used to modulate potassium-
CC chloride cotransport in a vertebrate. Therapeutic compositions
CC comprising modulators of the activity of KCC (preferably antibodies or
CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
CC anaemia, and hypertension (also via gene therapy using the KCC
CC polynucleotide). The present sequence encodes a KCC of the invention.
XX
XX Sequence 5239 BP; 1015 A; 1612 C; 1560 G; 1049 T; 3 other;
SQ
Query Match 33.3%; Score 1418; DB 22; Length 5239;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;
OY 483 GACGACATAGAAAGCTCGAAATGCTTATCTCAATAATTCCTCAATGAGAGAGAT 542
DB 131 GATGAAATCCAAAGAAAGAAAGAGCCATTCNTCAACATGTCGAGGTGGAACAGAGAGC 190
OY 543 GAATATTTTGATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGAGCCGAGGTG 602
DB 191 TTCTTTGAAGGGAAGAAATGGCACTTTTCGAGGAGAGATGGACAGTAACCCCATGGTG 250
OY 603 TCTTCCCTCCCAACCGCATGSCCAATACACTAATCTGACTCAAGGAGCAAGAAACAT 662
DB 251 TCCTCGCTGNTCAACAGCTGGCCAACTACACCAACCTGAGCCAGGGCGTGGTGAGCAC 310
OY 663 GAAGAGGAGAAACATCACTGAAGGGGAAAGAGAGCCCAACAGACCCCGCAATGGGT 722
DB 311 GAGGAGGAGAGAGAGCGCGGGGGA-----GGCCAAGGCTCCGGCATGGGC 361
OY 723 ACCTTCATGGGTGTACTCTCCCATGTCTACAAATATTTTGGAGTATCTTTTPTTA 782
DB 362 ACCTTCATGGCGTGTACTGCGGTGCTGAGAAACATCTCTGGGGGTCTCTCTCTG 421
OY 783 CGCCTTACATGGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGGCAATGTCTTATC 842
DB 422 CGCCTGACGTGGATCGTGGGGGTGGTGTCTCTGGAGTCTCTCTCATCTGGGCCATG 481
OY 843 TGCTGCTGTGTACAAATGTTGACTGTCTATCTCCATGAGTGGCATTTGCCACTAATGGAGTG 902
DB 482 TGCTGCACATGTACAACTGTGACCGCCATTTCCATGAGTGGCATCTGCTACCAACGGTGTG 541
OY 903 GTGCCAGCTGGGGGTCTACATCTTTAATGATTTCCGGGCACTGGGCCAGAGTTTGGTGGG 962
DB 542 GTCCAGCTGGCGGTCTCTACTACATGATATCGCGCTCGCTGGGAGCCAGTTTGGAGGC 601
OY 963 GCTGTGGCCTCTGCTTTTATCTTGGTACCACATTTGGCAGGCAATGATACCTCTGGT 1022

DB 602 CTTGTGGCCTCTGCTTCTACTGGGACAGAGCTTTTGCAGGGGCAATGATATATTTTGGGG 661
OY 1023 GCCATTGAAATCTTTTCTGCTATATCGTCCCGAGCTGCCATCTTTTCACAGTGTATGAC 1082
DB 662 ACCATCGAGATTTTCTGACGTACATCTCCCGGTGGGCACTTTCCAGCGGAGGT 721
OY 1083 GCATCAAGGAATCAGCAGCCATGCTAAATAACATGCTGTCTACGGGACAGCTTTCTTGG 1142
DB 722 GCAGGTGGCGAGGCGCGCCATGTCACAAACATGCTGTGTAGCGGACAGTGCACGCTC 781
OY 1143 GTCTTATGTTAGTGGTATTTTATGGCGCTACGCTATGTAACAAAGTTTGCCTCANNT 1202
DB 782 GTGCTATGGCCCTGGTGGTCTTCTGTTGGGCTCAAGTATGTAACAACTGGCGTGTGTC 841
OY 1203 TTCTGGCCTGTGTCTATTTGCTCATCTTGCCCATCTATGCTGGAGCCATCAAGTCTTCT 1262
DB 842 TTCTGGCCTGTGTCTGCTGCTCATCTGCGCATCTATGCGGCGTCTCAAGTCTGCC 901
OY 1263 TTGCTCTCCACACTTCCCGGTCTGCATGCTGGGTAAACCGCACTCTTTTCATCAAGACAC 1322
DB 902 TTCAGCCCGCGGACATCCCGGTCTGCTCTGCGGAAACCGCACGCTGTACGCGCGAGC 961
OY 1323 ATTGAGGTTTGTCTTAAGACCAAGAAATTAACAACTAGCAGTCCCATCAAGTATGAG 1382
DB 962 TTCGATGCTGCTCAAGGCTTACGGCATCCAAACAACTCAGCCACCTCCGCGCTCTGG 1021
OY 1383 GGATTTCTGTAACTCGAGTCAATTTTCAATGCCACCTGTGATGATATCTTTGTTTCCAC 1442
DB 1022 GGCCTCTTCTGCAACGGCTCCCA--GCCAGCGCGCTGTGACGAGTACTTTCATCCAG 1078
OY 1443 AATTAAGTCACTTCAATCCAGGCAATCTCTGGATTTGGTGTGTTAATTTACAGAGAA 1502
DB 1079 AACAACTCAACGAAATCCAGGCAATCCCGGCGCGGCGAGTGTCTTCTCTGGAGAAC 1138
OY 1503 CTTTGGAGTAAATTAACCTACCAAGGGAGAGATCATCGAABA-----GCCTTCAGCC 1553
DB 1139 CTGTGGAGTACGTACGGCACCGCGGGCGTGTGTGGAGAAAGAGTGTGCCCTCGGTG 1198
OY 1554 AAATCTTCTGATGTCTTAGGCAGCTTAAACCAATATATGTTTCTTTGTGACATCACCA 1613
DB 1199 CCGGTGCGAGGAGAGCGGTGCCAGCACACTGCGCTACGTCACCGACATCGCGGCC 1258
OY 1614 TCCTTCAAGTCTGTGGTGGAAATCTTCTTCTCTCTGTGTACAGGTATCATGGCTGGATCA 1673
DB 1259 TCCTTCAAGTCTGTGGTGGTGTCTTCTTCTCTGCGTACCGGTATCATGGCGGTTC 1318
OY 1674 AACAGATCTGAGATCTGAAGATGCTCAGAGTCTATTCGATTTGTTGATCTATCTTGGC 1733
DB 1319 AACCGTCCGGGAGACCTCAAGGATGCACAGAGTCCATCCCCACGGGACCATCTTGGCC 1378
OY 1734 ATCTGACCACTCTTCTTGTGTTTATTTAAGCAATGTTGTCCTTTTGTGTCATGTTGAA 1793
DB 1379 ATAGTGAGGAGCTTCTTCACTATCTCTCTGCAATGTGCTGTTTGGGCGCTGCATGAA 1438
OY 1794 GGGTGTGTTCTCAGAGACAAGTTCGGTGTGCTGTGAAAGTAAATTTGGTGGTAGGAC 1853
DB 1439 GGGTGTGTTCTACAGATAAGTTCGGGAGGCGCTGCGAGGGAACCTGGTCTATCGGCA 1498
OY 1854 TTATCTTGGCCATCCCATGGTGTATTTTATGGCTCTTCTTTTCAACATGTTGGGCT 1913
DB 1499 CTGGCCTGGGCGCTCCCTCTGGGTCTATGTCATGGCTCTTCTTCTCCACCTGGGTGCC 1558
OY 1914 GGACTTCAGAGCTTCAGAGTGCACCGAGGCTGTCTACAGCTATTTGCCAGGATAACATC 1973
DB 1559 GGCCTGAGACCTTCAGGGGACCGGCTACTGAGGCGCATTTGCCGTGAGCGGATC 1618
OY 1974 ATACCGTTCTGAGGTTTGTGGCCACAGCAAGCCAAATGGGGAACCTTACTGGGCTTTA 2033
DB 1619 GTCCCTCTCTGAGGTGTTTGGCCACGGGAAGCCAAACGGGAGGCCCACTGGGCGGTG 1678
OY 2034 CTTCTAAGTCTGCCATTTGAGAGCTTGGATACTCATTTGCTCTCTTCTTGTGGCC 2093
DB 1679 CTGCTGACAGTCTCATCTCGGAGTGGCATCCTCATCGCTCTCTCTGGAGAGCGTGGCC 1738

Qy	3174	ATCGGGCTATCCAAAACACAGACGACAGAGAGGCAAAATTTGGTGAAGACCCGAAACTCA	3233
Db	2819	ATCGAGCTGTCCAAAGAACACGACGACGAGGAGCCAGCTGATCCACGACGAGAAACACC	2878
Qy	3234	ATGCTACGATTGACACGACGATTTGGCTCTGATGAGGACGAAAGACAGAAACCTTATCAGGAG	3293
Db	2879	GC-----GTCCACACCCGGCGGCGACGCCAGACCCACGCGCGCTACGCCAGAC	2929
Qy	3294	AAGGTGCACATGACTTTGGACAAAAGACAAAGTACATGGCATCCCGG---GGACAAAAGCG	3350
Db	2930	AAGGTGCAGATGACCTGGACCCAGGAGAGCTGATCGCTGAGAAGTACAGGACGACAGAC	2989
Qy	3351	AAGTCAATGAAGATTCACGAGACCTGCTTAAACATGCGTCGTCGGACACAGTCCCATGTGAGG	3410
Db	2990	ACCAGCCTATCCCGTTTCAAAGACCTCTTCAGCATGAAGCCCGGACCCAGTCCAAACGTCAGG	3049
Qy	3411	CGGATGCATACAGCAGTGAACCTCAACGAGTTTATAGTTAAACAAGTCCCACATGAAGCAAAG	3470
Db	3050	CGGATGCACACGGCTGTGAAGCTCAATGGCTCGTCNTCAAAGTCCCAGGATGCGCAG	3109
Qy	3471	CTGGTTTATTGTAATATGCCAGGCGCCACCCGAAACCTTGAGGGTGATGAAAACCTACATG	3530
Db	3110	CTGGTCTCTGCTCAACATGCCAGGTCTCTCCCAAAAACCGGCAGGAGACGAGAACTACATG	3169
Qy	3531	GAGTTCCTAGAGTGCTTACCGAGGAGACTAGACGGAGTCTCTACTTTGTCGGGGTGGTGGC	3590
Db	3170	GAGTTTCTTGAAGTCTCTGACCGAGGGGCTGAACAGAGTCTCTCTGTGAGGGGTGGCGGC	3229
Qy	3591	AGTGAAGTGATCACCATTATTATCATAA	3617
Db	3230	CGGAGGTGATCACCATCTACTCTCTAA	3256
RESULT 11			
AAKS1667			
ID	AAKS1667 standard; cDNA; 5263 BP.		
XX	AAKS1667;		
AC			
DT	06-NOV-2001 (first entry)		
XX	Human polynucleotide SEQ ID NO 212.		
DE			
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157190-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	05-FEB-2001; 2001WO-US04098.		
XX			
PR	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693345.		
PR	30-NOV-2000; 2000US-0728422.		
XX			
XX	(HYSE-) HYSEQ INC.		
PA			
PI	Tang YT, Liu C, Drmanac RT, Auandi V, Zhou P, Xu C, Cao Y, Ma Y;		
PI	Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WPI: 2001-476283/51.		

XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS
XX Claim 1; Page 1034-1039; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK8020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 5263 BP; 1018 A; 1625 C; 1570 G; 1050 T; 0 other;
Query Match 33.3%; Score 1417.8; DB 22; Length 5263;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 2105; Conservative 0; Mismatches 1009; Indels 33; Gaps 5;
QY 483 GACGGACATAAGAAAGCTCGAATGCTTATCTCAATAATTCCTCAATGGAAGAGAT 542
DB 150 GATGGAATCCAAAGAAACAGCCATTCCTCAACATGTCGAGGTGGAACAGAGAGC 209
QY 543 GAATATTTGATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGTG 602
DB 210 TTCTTTGAAGGAAGAAATGTCACCTTTTCGAGGAGGAGATGGACAGTAACCCCATG 269
QY 603 TCTCTCCCTCAACCGCATGCGCAATACATTAATCTGACTCAAGGAGCAAGAGACAT 662
DB 270 TCTCGTCTCAACAGCTGCGCAATACACCAACCTGAGCGAGGCGTGTGGAGCAC 329
QY 663 GAAGAGGCGAAACATCACTGAAGGGAAGAAAGACCCACCAAGACCCCAATGGGT 722
DB 330 GAGGAGGAGGAGAGCGCGCGGGA-----GGCCAGGCTCCGCGCATGGC 380
QY 723 ACCTTCATGGGTGTCTACCTCCATGTCTCAAAAATATTTTGGAGTGAATCTTTTATA 782
DB 381 ACCTTCATGGGTGTCTACCTCCATGTCTCAAAAATATTTTGGAGTGAATCTTTTATA 440
QY 783 CGCCTTACATGGGTGTGGGACAGCTGGAGTCTTCAGGCTTTTGGCAATGTCCTTATC 842
DB 441 CGCCTTACATGGGTGTGGGAGTCTTCAGGCTTTTGGCAATGTCCTTATC 500
QY 843 TGCTGCTGTGTAATGTTGACTGTATCTCCATGAGTGGCATTTGCCACTAATGGAGTG 902
DB 501 TGCTGCACATGTACAATGCTGACCGCCATTTCCATGAGTGGCATCTTCCAAACGGTGT 560
QY 903 GTGCAGCTGGGGGTCTATCTTTATGATTTCCCGGCACTGGGCGGAGAGTTGGTGG 962
DB 561 GTCCAGCTGGGGGTCTCTACTACATGATATCGCGTCTGGGACCCGAGTTTGGAGGC 620
QY 963 GCTGTGGCTCTGCTTTTATCTTGGTACCAATTTGGCAGAGCCATGTACATCTTGGT 1022
DB 621 GCTGTGGCTCTGCTTTTATCTTGGTACCAATTTGGCAGAGCCATGTATATTTGGGG 680
QY 1023 GCCATGAAATCTTTTCTGTGTATATCGTCCCGAGTGGCATCTTTACAGATGATGAC 1082
DB 681 ACCATCGAGATTTTCTGAGCTACATCTCCCGGTGGCGCATCTTCCAGCGGAGGCT 740
QY 1083 GCATCAAGGAATCAGCAGCCATGTAAATAACATGCGGTCTACGGCAGAGCTTTCTTG 1142
DB 741 GCAGGTGGCGAGGCGGCCATGCTGCACACATGCGTGTGTACGGCAGGTGACGCTC 800
QY 1143 GTCTTATGGGTATAGTGTATTTATCGGCTACCGCTATGTAACAAAGTTTGCCTCAT 1202

DB 801 GTGCTCATGGCCCTGGTGGTCTTCTCGTGGCGCTCAAGTATGTCAACAAGCTGGCGCTGTC 860
QY 1203 TTCTGGGCTGTGTCAATTTGTCTCCATCTTGCCATCTATGTGGAGCCATCAAGTCTTCT 1262
DB 861 TTCTGGGCTGGTGTGTCTCCATCTGCGCCATCTATGCGCGGTCTATCAAGTCTGCC 920
QY 1263 TTTGCTCTCCACACTTCCCGGTCTGCATGCTGGGTAAACCGCACTCTTTTCATCAAGAC 1322
DB 921 TTGACACCCCGGACATCCCGGTCTGCGCTCTCTGGGAAACCGCACGCTGTACGGCGCAGC 980
QY 1323 ATTGACGTTTCTCTTAAGACCAAGAAATTAACAACATGACAGTGCACATCAAAAGTTATGG 1382
DB 981 TTGATGCTGCTGGTCAAGCCCTACGGCATCCACAACACTCAGCCACCTCCGCGCTCTGG 1040
QY 1383 GGATTTCTGTAACTCGAGTCAATTTTCAATGCCACTGTGTATGAATATCTTTTTCAC 1442
DB 1041 GGCCTCTTCTCAACGGCTCCCA---GCCAGCGCGGCTGTGACGAGTACTTTCATCCAG 1097
QY 1443 AATAACGCTCACTTCAATCCAGGCAATTCCTGGATGGCTAGTGTATTAATTTACAGAGAT 1502
DB 1098 AACAAAGTCAACCGAAATCCAGGCAATCCCGGCGCGGCGAGTGTCTTCTCTGGAGAAC 1157
QY 1503 CTTTGGAGTAATTAACCTACCAAGGAGAGATCATCGAAAA-----GCTTTCAGCC 1553
DB 1158 CTGTGGAGTACGTACGGCACGCGGGCGGTTTGTGGAGAAAGAGTGTGCCCTCGGTG 1217
QY 1554 AAATCTTCTGTATGCTTTAGGAGCTTAAACCATGAATATGTTTGTGTGACATCAACACC 1613
DB 1218 CCCGTGGCAGAGAGAGCGGTCGACGACACTGCGCTACGTGCTCACCGACATCGCGGCC 1277
QY 1614 TCCTTCAGCTTCTGTGGGAAATCTTCTTCCCTCTGTGTACAGGTATCATGGCTGGATCA 1673
DB 1278 TCCTTCACTCTGCTGGTGGCATCTACTTCCCTGACCGGTATCATGGCGGTTCA 1337
QY 1674 AACAGATCTGAGATCTGAAAGATGCTCAGAAAGTCTATTCCGATTTGGTACTATCTCTGCC 1733
DB 1338 AACCGTCCGGGACCTCAGAGATGCACAGAGTCCATCCCAACGGGACCATCTCTGCC 1397
QY 1734 ATCTGACCACTCTCTTTTATTAAGCAATGTTGTCTTTTGGTGCATGTATTGAA 1793
DB 1398 ATAGTGACGAGCTCTTTCATCTATCTCTCTGCTATGCTGTTTGGGCGCTGCATTGAA 1457
QY 1794 GGGTGTCTCAGACAGCAAGTTCCGTGATGCTGTGAAGTAATTTGGTGGTAGGCACC 1853
DB 1458 GCGTGTGCTTACAGATTAAGTTCCGGGAGGCCCTCGCAGGGGAAACCTGGTCTATCGGCATG 1517
QY 1854 TTATCTTGGCCATCCCATGGGTGATTTGTTATTCGCTCTCTTTTCAACATGTGGGCT 1913
DB 1518 CTGGCTGGCCCTCCCTCGGTGATCTGTCATCGGCTCTCTCTCTCCACCTCGGCGCC 1577
QY 1914 GGACTTCAGAGCTTCACAGGTGACCGAGGCTGTCTACAAGCTATTGGCAAGGATAACATC 1973
DB 1578 GGCCTGCAGACCTTCACGGGGCACCGGCTACTCTGAGGCCATTGGCCGTGACGGCATC 1637
QY 1974 ATACCGTTTCTGAGGTTTGGCCACAGCAAGCAATGGGGAACTTACCTGGGCTTTA 2033
DB 1638 GTCCCTTCTCTGAGGTGTTTGGCCACGGGAAGCCAAACGGGAGCCACACGTGGGCGCTG 1697
QY 2034 CTTCTAATCTGCTGACAGCTTGGATACCTCATTTGCTCTCCCTCCCTGGATCTTGTGGCC 2093
DB 1698 CTGTGACAGTCTCATCTGCGAGCTGGCATCTCATCGGCTCTCTGGAAGCGGTGGCC 1757
QY 2094 CCAATCTCTTCATGTTTCTCATGTTGTACCTCTTTGTAAACTTTGGCATGTGCCCTTG 2153
DB 1758 CCGATCTCTCCATGTTCTCTCTCATGTTGTACCTGTTGTGAACCTGGCTGGCGGTG 1817
QY 2154 AAAACATTTCTCGAAACCAACTGGAGACCCCGATTCGCGCTACTACCATTTGGGCGCTT 2213
DB 1818 CAGACCTGTCTACGTACCCCAACCTGGCGTCCAGCTTCAAGTTCTACCACTGACACCTG 1877
QY 2214 TCTTTTATGGAATGAGTATCTGTCTGCTGTGATGTTTCTTCTCTCTGATATATGCC 2273
DB 1878 TCCTTTCTGGGTATGAGCCCTGTGCTCGCGCTGATGTTCTCTCTCTCTGCTCTCTGCTG 1937

CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness.
 CC auto-immune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.

XX
 SQ Sequence 5261 BP; 1019 A; 1625 C; 1568 G; 1049 T; 0 other;

Query Match 33.2%; Score 1416.2; DB 22; Length 5261;
 Best Local Similarity 66.9%; Pred. No. 0;
 Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;

QY 483 GACGACATAGAAAGCTCGAAATGCTATCTCAATAATTCATAATTAAGAAGAGAT 542
 DB 150 GATGAAATCCAAAGAGAAACAGCCATTCCTCAACATGTCGAGTGGACACAGAGAGC 209
 QY 543 GAATATTTGATAAAATTTGGCACTTTTGAGGAAGAAATGGACACCGAACGAGGTG 602
 DB 210 TTCTTTGAAGGGAAGAACATGCACTTTTCGAGGAGGAGATGACAGTAACCCATGTTG 269
 QY 603 TCTTCCTCCTCAACCGCATGCGCAATTTACATACTGACTCAAGGAGCAAGAAACAT 662
 DB 270 TCCTCGCTGCTCAACAAGCTGGCCAACTACACCAACCTGAGCCAGGGCGTGGTGAGCAC 329
 QY 663 GAAGAGGCGAAGAAACATCACTCAAGGGAAGAAAGCCACCAAGACCCCAATGGGT 722
 DB 330 GAGGAGGACGAGAGAGCGCGCGGGG-----GGCCNAGGCTCCGCGCATGGGC 380
 QY 723 ACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCTCTTTTATA 782
 DB 381 ACCTTCATCGCGGTCTACCTCGCGTCCCTGCGAGACATCTCGGCGTCATCTCTTCCTG 440
 QY 783 CGCCTTACATGGGTGGTGGGACAGCTGGAGTTCTTCAGGCTTTTGGCAATGTCCTATC 842
 DB 441 CGCCTGAGCTGGATCGTGGGGGTGGTGGTGTCTCTGAGTCTCTCTCATCTGCGCCATG 500
 QY 843 TGCTGCTGCTGACAAATGTTGACTGCTATCTCCATGAGTGCCATGCGCAATATCGAGTG 902
 DB 501 TGCTGCAATGACAAATGCTGACCCGCAATTCATGAGTGGCATCGCTACCAACGGTGTG 560
 QY 903 GTGCCAGCTGGGGGTCTACTTTATGATTTCCCGGGCACTGGGCGCCAGAGTTTGGTGGG 962
 DB 561 GTCCCAGCTGGGGGTCTCTACTACATGATATCGCGCTCGCTGGGACCCGAGTTTGGAGGC 620
 QY 963 GCTGTTGGCCTCTGCTTTTATCTTGGTACCACATTTTGCAGAGCCATGTACATCCTTGGT 1022

DB 621 GCTGTCGGCCTCTGCTTCTACTCTGGGACGAGCTTTGAGGGGCCATGTATATTTGGGG 680
 QY 1023 GCCATTGAAATCTTTCTGGTCTATATCTGCCCCGAGCTGCCATCTTTACAGATGATGAC 1082
 DB 681 ACCATCGAGATTTTCTGACGTACATCTCCCGGGTGGGCCATCTTCCAGGGGGAGGT 740
 QY 1083 GCATCAAGGAATCAGACGCAATGTAATAACATGCGTGTCTACGGCACAGCTTTCTTTG 1142
 DB 741 CGAGGTGCGAGGCGCGGCCCATGTGTCACAAACATGCGTGTGTACGGCACGTCACGCTC 800
 QY 1143 GTCCTTATGATATAGTGGTATTTATCGGCTGACGCTATGTGAACAAGTTTGCCTCANVT 1202
 DB 801 GTGCTCATGGCCCTGGTGGTCTTCGTGGCGTCAAGTATGTCAACAAGCTGGCGTGGTC 860
 QY 1203 TTCTGGGCTGTGTCATTTGTGTCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCT 1262
 DB 861 TTCTGGGCTGGTGGTGTGTCATCTGTCATCTGCGGCATCTATGCGGGCTCATCAAGTCTGC 920
 QY 1263 TTGCTCTCTCACACTTCCCGTCTGCAATGCTGGTAAACCGCACTCTTTTCATCAAGACAC 1322
 DB 921 TTCCAGCCCCGGACATCCCGTCTGCTCTCTGGGAAACCGCACGCTGTACGGGCGACG 980
 QY 1323 ATTGACGTTTCTCTTAAGACCAAGAAATTAACACATGACAGTCCCATCAAGTATGG 1382
 DB 981 TTCGATGCTCGTCAAGGCCCTACGGCATCCACAACTCAGCCACCTCCGCGCTCTGG 1040
 QY 1383 GGATTTCTCTGTAATCTGAGTCAATTTTCAATGCCACTGCTGATGAATACTTTGTTTCA 1442
 DB 1041 GGCCTCTTCTGCAACGGCTCCCA---GCCAGCGCGCTGTGAGAGTACTTTCATCCAG 1097
 QY 1443 AATAACGTCACCTCAATCCAGGCACTCTCGATTTGGTGTAGTGTATTAATACAGAGAT 1502
 DB 1098 AACACGTCACGAAATCCAGGGCATCCGGCGCGCGGCGAGTGTCTTCTCTGGAGAAC 1157
 QY 1503 CTTTGGAGTATTAACCTACCCAAAGGAGAGATCATCGAAA-----GCCTTCAGCC 1553
 DB 1158 CTGTGGAGTACGTACGCGCACGCGGGGCGTTTGTGGAGAAAGAAAGGTGTGCCCCCTGGTG 1217
 QY 1554 AAATCTCTGATGCTTTAGGCGCTTAAACCATGAATATGTTTGTGTGACATCAACACC 1613
 DB 1218 CCGTGGCAGAGGAGAGCGCGTCCAGCACATGCGCCTAGTGCTCACGACATCCGGGCC 1277
 QY 1614 TCCTTCACGCTTCTGGTGGAAATCTTTTCCCTCTGTTACAGGATCATGSGCTGGATCA 1673
 DB 1278 TCTTCACTGCTGTTGGCATCTACTTCTCCGTGACCGGTATCATGSGCGGTTCA 1337
 QY 1674 AACAGATCTGAGATCTGAAAAGATGCTCAGAAAGTCTATTCGATTTGGTACTATCTCTGCC 1733
 DB 1338 AACCGGTCCGGGACCTCAAGGATGCAAGAGTCCATCCCAAGGGGACCATCTCTGGCC 1397
 QY 1734 ATCTGACCACTCTCTTTGTTTATTTAAGCAATGTTGCTCTTTTGGTGGCATGTTGAA 1793
 DB 1398 ATAGTGACAGCTCTTTTCATCTATCTCTCTGCAATGTGCTGTTTGGGGCTCGCATGAA 1457
 QY 1794 GGGGTGTTCTCAGAGACAAGTTCGGTGATGCTGTGAAGGTAAATTTGGTGGTAGGCACC 1853
 DB 1458 GCGGTGTTCTTACAGATAAGTTCGGGAGGCCCTGCGAGGGGAACCTGTCATCGGCATG 1517
 QY 1854 TTATCTTGGCCATCCCATGAGTGTATTTGGCTCTCTCTTTTCAACATGTGGGGCT 1913
 DB 1518 CTGGCCTGGCCCTCCCTCTGGGTCTATGTCATCGGCTCTCTTCTTCCACCTCGGGTGC 1577
 QY 1914 GGACTTCAGAGCCTCAGAGTGCAAGGCTGCTACAAGCTATTTCGCAAGCAATAACATC 1973
 DB 1578 GGCCTGCAGACCTCTACGGGGCACCGGCTCTACTGAGGCCATTTGCCGTGACGGCATC 1637
 QY 1974 ATACCGTTCTGAGGGTTTTTGGCCACAGCAAGAACCAATGGGGAACCTTACCTGGGCTTTA 2033
 DB 1638 GTCCCTCTCTGCAAGTGTGTTGGCCACGGGAAGCCAAACGGGAGCCACCGTGGCGCTG 1697
 QY 2034 CTTCTAATCTGCTGCATTTGACAGCTTGGAAATATCTATTGCTCTCCTGGATCTTTGTGCC 2093

Db 1698 CTGCTGACAGTCTCATCTGCGAGACTGGCACTCTCATCGCCTCTCTGGACAGCGTGGCC 1757
Qy 2094 CCAATCTCTTCCATGTTTTCTCATGCTGTACCTCTTTGTAAACTTGGCATGTCCCTTG 2153
Db 1758 CCGATCCTCTCCATGTTCTCTCATGCTGTACCTGTCTGTGAACTGTGCGCTTGCCTCGTG 1817
Qy 2154 CAAACATTTACTTCGAACACCCCACTGGAGACCCGATTCGCTACTACCAATTTGGGCCCTT 2213
Db 1818 CAGACCTCTACTAGTACCCCACTGGCGTCCACGCTTCAAGTCTTACCACTGGACCTG 1877
Qy 2214 TCTTTCATGGGAATAGATATCTGTCTGGCTCTGATGTTCAATTTCTTCTGGTATTATGCC 2273
Db 1878 TCTTTCTGGGTATGAGCTGTGCTTGGCGCTGATTTCACTGTCTCTGTGTAACGCG 1937
Qy 2274 ATTGTAGCCATGGTAATAGCTGATGATCAAGTACATTAAGTAAATCAACAGAGCTGAG 2333
Db 1938 CTGTCCGCCATGCTCATCGCTGGCTGCTCAAGTACATCGATGACCGCGGGCCGAG 1997
Qy 2334 AAAGAAATGGGGTATGTTATCCGTGGCTGTCCCTCAGTGCAGCCCGGTTTCTTGTGTT 2393
Db 1998 AAGGAGTGGGGCGATGGCATCCGTGGCTATCCCTGAACGCCCGCTACGCCCTGTCTG 2057
Qy 2394 CGATTGGAGAGGACCTCCACACTAAAACTGGAGGCCCTCAGTTGCTTGTATTAATG 2453
Db 2058 CCGGTGGAGCAGCGTCCCCCCACACCAAGAACTGGAGGCCCCAGGTGCTGTGATGCTG 2117
Qy 2454 AAATAGATGAGACTTACATGTCAAGCATCTCGCCTCTCACCTTTCCTCAGAGTCTC 2513
Db 2118 AACCTGGACGGGAGCAGGCATGAAGCACCCCGCTCTGTCTTCACTGCTGAGCTG 2177
Qy 2514 AAAGCAGGAAAGGTTACTATTGTGGCTCTGTCTCATCTGTGGGAACTTCTCTAGAGAAC 2573
Db 2178 AAGCCCGCAGAGGCTGACCATCTGGCTCGTCTGGAGGAGCTACCTGGACAG 2237
Qy 2574 TAGCGTGAAGCTTTAGCTGTGAGCAGACATAAAGCACTAATGAGGAGCAGAGAGTGA 2633
Db 2238 CACATGAGGCTCAGCGGGCCGAGGAGAAACATACGGTCTCCCTAATGAGCAGACAGAGACC 2297
Qy 2634 AAGGATTTCTGCAGCTGTGGTGGCCGCGCAGCTGAGAGAGGCAATTTCCACCTCATC 2693
Db 2298 AAGGGCTTCTGCAGCTGTGGTGTCTGTCCAGCTCGGGATGGCATGTCCACCTGTATC 2357
Qy 2694 CAGTCATGTGGCTTGGGGCATGAAGCAACACACGCTGTGTATGGGCTGGCCTAATGCC 2753
Db 2358 CAGTCGGCGCTTGGCGGCTTGAAGCAACACACGCTGTCTATGCTGTGGCCGCGATCC 2417
Qy 2754 TGGCGTCAAGAGCAAGATGCCCGCTTGAAGACTTTTATTTGGCACAGTTGAGTGAACA 2813
Db 2418 TGAAGCAGGAGGACAAACCCCTTCTCTGGAAGAACTTTGTAGACACCCGTCGCGACACC 2477
Qy 2814 ACTGCTGCCATCTTGCACCTGCTGGTGGCTAAGCAATCTCTTCTCCAGCAATGTG 2873
Db 2478 ACCGCCGCGCACAGGCTCTGCTGGTGGCCAGAACGTCGACTCGTTTCCGCAAAACCCAG 2537
Qy 2874 GAGCAATTTTCTGAGGCAACATTTGATGTGTGGTATTTGTGATGATGGGGGATGCTT 2933
Db 2538 GAGGCTTCGGCGGGCCACATCGAGTGTGTGGATCTGTGACACGCGCGCATGCTC 2597
Qy 2934 ATGCTACTACATTTCTTACTGAACACAGCAACAGGTGTGGCGAAAGTGCAGCATACGGATC 2993
Db 2598 ATGCTGCTCCCTTCTCTGCTGCGCCAGCAACAGGTGTGGAGGAAGTCCCGGATGCGTATC 2657
Qy 2994 TTCACAGTACCCCAATTTAGAGCAACAGTATCCAAATGAAGAGGACCTAGCCACTTC 3053
Db 2658 TTCACCGTGGCCAGGTGGACGACAAACAGCATCCAGATGAAGAGGACCTGCAAGTGTTC 2717
Qy 3054 CTATATCACTTACCGCATTTGAGGGGAGGTAGAAGTGTGGAGATGATGATGACAGTATATA 3113
Db 2718 TTGTACCATTTGGCATCAGCGCCGAGGTGGAGTGTGTGGATGTTGAAACGACATA 2777
Qy 3114 TCAGCATATCTTACGAGCGCACTTTTATGATGATGAACAAAGGTCCAGATGCTTCGGCAC 3173
Db 2778 TCTGCTTTCACCTACGAGGACACTAATGATGAGCAGAGGTTCGAGATGCTGAAGCAG 2837

Qy 3174 ATGGCGCTATCCAAAACAGACGAGCAGAGCAGACGACAAATTTGGTAAAGACCGAAACTCA 3233
Db 2838 ATGCAGCTGTCCAAAGAACGACGAGCAGAGCGCCAGCTGATCCACGACAGGAACACC 2897
Qy 3234 ATGCTACGATTGACAGCAITTTGGCTCTGTATGAGGACGAGAGACGAAACCTATCAGGAG 3293
Db 2898 GC-----GTCCACACCGCGCGGCGAGCCAGGACCCAAAGCGCCCTACGCCAGAC 2948
Qy 3294 AAGTGCACATGACTTGGACAAAAGACAAAGTACATGGCATCCCG- --GGACAAAAGCG 3350
Db 2949 AAGGTGCAGATGACTTGGACCAGGAGAAAGCTGATCGCTGAGAAGTACAGGAGCAGAC 3008
Qy 3351 AAGTCAATGGAAGGATTCAGGACCTGTTAAACATGCGTCCGAGCAGTCCCAATGTGAGG 3410
Db 3009 ACCAGCCTATCTGGTTTCAAGACCTCTTCAGCATGAAGCCGACCACTCCAAACGTGAGG 3068
Qy 3411 CGGATGCATACAGCAGTGAACCTCAACGAGGTTATAGTTAAAGTCCATGCAAGCAAG 3470
Db 3069 CGGATGCACACGGCTGTGAAGCTCAATGGCTGCTCTCAACAAGTCCAGGATCGCAG 3128
Qy 3471 CTGGTTTATTTGAATATGCCAGGGCCACCCGAAACCTGAGGGTGTGAAAACCTACATG 3530
Db 3129 CTGGTCTCTGCTCAACATGCCAGGTCCTCCAAAACCCGCGAGGAGACGAGAACTACATG 3188
Qy 3531 GAGTTCCTAGAGGTGCTTTACCGAGGGACTAGAGCGAGTCTTACTTTGTCGGGGTGTGGC 3590
Db 3189 GAGTTCCTTGAAGTCTCTGACCGAGGGCTGAACAGAGTCTCTCTGTCAGGGGTGGCGC 3248
Qy 3591 AGTGAAGTGAATCACCATTATTATATAA 3617
Db 3249 CGGGAGGTGATCACCATCTACTCTCTAA 3275

RESULT 13

AA559393
ID AA559393 standard; cDNA; 5155 BP.

XX AC AA559393;

XX DT 16-JAN-2002 (first entry)

XX DE Mouse cDNA encoding potassium-chloride cotransporter KCC4.

XX KW Mouse; ss: potassium-chloride cotransporter; epilepsy; hypertension;
KW KCC; hypotensive; anticonvulsant; antianaemic; sickle-cell anaemia;
KW gene therapy.

XX OS Mus sp..

XX PN WO200179525-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US12395.

XX PR 14-APR-2000; 2000US-197350P.

XX PA (UYVA-) UNIV VANDERBILT.
XX PA (GAMB/) GAMBA G.

XX PI Gamba G, Mount DB, Delpire E, George AL;

XX DR WPI; 2001-611726/70.

XX DR P-PSDB; AAU39098.

XX PT New isolated and purified potassium-chloride cotransporter polypeptide
PT for detecting a modulator of potassium-chloride cotransporter that can
PT treat epilepsy, sickle cell anaemia, and hypertension -

XX PS Claim 24; Page 279-287; 352pp; English.

XX CC The invention relates to an isolated and purified, biologically active

CC KCC2, KCC3, or KCC4 potassium-chloride cotransporter polypeptide
 CC and polynucleotides encoding them. KCC and the nucleic acid encoding KCC
 CC are used to produce an antibody against KCC, which can be used to detect
 CC KCC. The antibody and nucleic acid are used in kits to detect KCC and
 CC the nucleic acid encoding KCC. KCC and nucleic acid encoding it are used
 CC to screen for candidate substances that can modulate the activity of KCC.
 CC KCC and the nucleic acid encoding it can be used to modulate potassium-
 CC chloride cotransport in a vertebrate. Therapeutic compositions
 CC comprising modulators of the activity of KCC (preferably antibodies or
 CC antisense oligonucleotides) are used to treat epilepsy, sickle cell
 CC anaemia, and hypertension (also via gene therapy using the KCC
 CC polynucleotide). The present sequence encodes a KCC of the invention.
 XX
 SQ Sequence 5155 BP; 1135 A; 1414 C; 1388 G; 1212 T; 6 other;

Query Match 33.2%; Score 1415; DB 22; Length 5155;
 Best Local Similarity 67.0%; Pred. No. 0;
 Matches 2092; Conservative 0; Mismatches 998; Indels 33; Gaps 5;

QY 508 CTTATCTCAATATTCATATGAGAGGAGATGATATTTGATATAAATTTGGCAC 567
 DB 224 CTTTCATCAATATGAGAGTGGAAAGAGAGAGCTACTTCGAGGGGAGAACATGGCAN 283
 QY 568 TCTTTGAGGAAGATGACACACGACCGAGGTCTTCCCTCTCAACCGCATGGCCA 627
 DB 284 TTTTGTGAGGAAGATGACACACCGACCGAGGTCTTCCCTCTCAACCGCATGGCCA 343
 QY 628 ATTACACTAATCTGACTCAAGGAGCAAGGAAACATGAAGAGGACGAAACATCACTGAAG 687
 DB 344 ACTATACCAACCTGAGCCAGGTGTGTAGACATGAGGAGATGAGGACA----- 394
 QY 688 GAAAGAGAGCCACCAAGACCCCAAAATGGGTACCTTCAATGGGTGTCTACCTCCCAT 747
 DB 395 GCGGAGGCGAGAGGTCAAGGCCCAACGATGGGCAACCTTCACTGGAGTCTACCTGCCGT 454
 QY 748 GTCTACAAATATTTTGGAGTGATCTTTTATAGGCTTACATGGGTGGTGGGCACAG 807
 DB 455 GCGTCAGAAACATCTTGGGTGTATCTTTTCCGCTGTGACCTGGATTTGGGGGCGAG 514
 QY 808 CTGAGGTCTTTCAGGCTTTTGCATTTGCTTATCTGCTGTCTGTATCAATTTTGTGACTG 867
 DB 515 CTGTGTATTGAGGCTTCTTCATTTGTTGGCATGTGCTGACCTGTATCAATGCTGACAG 574
 QY 868 CTATCTCAATGATGCCATGTCACATAATGAGTGGTGGCCAGTGGGGCTCATACTTTA 927
 DB 575 CCATCTCAATGAGCCCATCGCTACCAACGGCGTGGTCCAGCGGGAGGCTCGTACTACA 634
 QY 928 TGATTTCCGGGCACTGGCCAGAGTTTGGTGGGGCTGTGGGCTCTGCTTTTATCTTG 987
 DB 635 TGATCTCCGTTTGGTGGGCGCTGAGTTGGAGGTGCTGTTGGGCTCTGCTTCTACTTGG 694
 QY 988 GTACCACATTTGACGACGATGATCATCTTGGTGCCATTTGGAATCTTTCTGGTCTATA 1047
 DB 695 GCACGACATTTGACGGCGCATGATACATCTGGGTACCATCGAGATCTTCTGACCTACA 754
 QY 1048 TGTGTCCTCCGAGCTGCCATCTTTCAAGTGTAGTACGCACTCAAGGAATCAGCAGCATGC 1107
 DB 755 TCTCTCCAAGTGGGCGCATCTTCCAGGCGAGAGACGGGCGATGGCGCGCCGACCTGT 814
 QY 1108 TAAATAACATGGGTCTACGGCAGAGTTTCTTGGTCTTATGATGATATGATGATTTA 1167
 DB 815 TGAACAACATGGGTGTATGGCAGCTGTGCCCTGGCACTCATGCGGCTGGTGTCTTTG 874
 QY 1168 TCGGGTACGCTATGTGAACAGTTTGTCTCANTTTTCTGCGCTGTCTATTGTGTCGA 1227
 DB 875 TTGTGTCAATAATGTCAACAGCTGGCACTGGTCTTCTTAGCTGTGTGTGCTTTCTA 934
 QY 1228 TCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTTGGTCTCTCCACACTTCCGGTCT 1287
 DB 935 TCTTGGCCATCTATGCTGGTGTATCAACAGAGCTTTGGCCCACTGACATCCGGTCT 994
 QY 1288 GCATGCTGGGTAAACCGCACTCTTTTCATCAAGACACATTTGAGCTTTGCTTAAGACCAAG 1347

DB 995 GCCTTCTAGGAAACGGCAGGCTGGCAATCCAAATTTGATACCTGTGCCAAGATGCGAGG 1054
 QY 1348 AAATTAACAACATGACAGTCCCATCAAAAGTTATGGGATTTCTTGTAACTCGAGTCAAT 1407
 DB 1055 TTGTGAGCAACGGTACAGTACACCATGTCACCTCTGGCGCTCTTCTGCAATG---GCTCCA 1111
 QY 1408 TTTTCAATGCCACCTGTGATGAATACCTTTGTTTCAATAACGTCACTTCAATTCAGGGCA 1467
 DB 1112 GCTTGGGTGCCACCTGTGATGAGTACTTTTGACAGAAACAAGCTTACTGAGATACAGGCA 1171
 QY 1468 TTTCTGGATTCGGTGTGATGAATAATACAGAGAAATCTTTGGAGTAATTTACCTACCCAAAGG 1527
 DB 1172 TCCCTGGTGTGGCAGTGGTGTCTTCTCGATACCTGTGGAGACATATTTCAAGACAAG 1231
 QY 1528 GAGAGATCATCGAAAA-----GCCTTCAGGCCAAATCTTCTGATGTCTTAGGCAGCT 1578
 DB 1232 GGGCATTTGTGAAAAAGAAAGGTGTCTCAGTGCCTGTGTCCGAGGAGAGCGCGCTG 1291
 QY 1579 TAAACCATGAATATGTTCTTGTTCACATCACCATCTCTTCAAGCTTCTGGTGGGAATCT 1638
 DB 1292 GTGATTTGCCATACGTCTCTCAAGACATCATGACCTACTTCCACCATGTAGTTGGCATCT 1351
 QY 1639 TCTTTCCCTCTGTACAGGTATCATGGCTGGATCAAAACAGATCTGGAGATCTGAAAGATG 1698
 DB 1352 ACTTCCGCTGTAACTGGGATCATGGCAGGATCCAAACGCTCCGGGACCTCAAGAGC 1411
 QY 1699 CTGAGAGTCTATTTCCGATTTGTTACTTCTTGGCATCTGACCACTCTCTTTGTTTAT 1758
 DB 1412 CCCAGAGTCTATTTCCAAACAGGACCATTTGCGCATCTGCTACTATCTTTTATTATN 1471
 QY 1759 TAAGCAATGTTGCTCTTTTGGTGCATGTATTGAAGGGTGTGTTCTCAGAGACAAGTTG 1818
 DB 1472 TTTCTCTGATAGTCTGTTTGGGCTGTCATTTGAAGGTGTAGTCTCTCGAGATAAGTTG 1531
 QY 1819 GTGATGCTGTGAAGAAATTTTGGTGTAGGACCTTATCTTGGCCATCCCACTGGGTGA 1878
 DB 1532 GGGAGGCTTTCGAAGGAAACCTGTGTCATTTGGCATGTGGCTTGGCCATCTCCCTGGGTCA 1591
 QY 1879 TTGTATTGGCTCTCTCTTTTCAACATGTGGGCTGGACCTTTCAGAGCCTCACAGTGCAC 1938
 DB 1592 TTGTATTGGCTCTCTCTCTTCTTCCACCTGTGGTGTGGCTGCAGAGCCTGACTGGGCAC 1651
 QY 1939 CGAGGCTGCTACAAAGCTATTGGCCAAAGGATAACATCATACCTTTCTGAGGGTGTG 1998
 DB 1652 CCCGCTACTGACAGGCAATTTGGCGGTGACGGAATCATCCCCCTCTCAGAGTGTG 1711
 QY 1999 ACAGAAAGCCAAATGGGGAACCTACCTGGGCTTTACTTCTAACTGCTGCCATTCAGAGC 2058
 DB 1712 ATGAAAAGGCCCAACGGGGAGCCCATGCGGCTGTGCTCACGGCTCTCATCTGTGAGA 1771
 QY 2059 TTGGAATACCTATTGCTCTCTCTGATCTTGTGGCCCAATTTCTTCCATGTTTTTCTCA 2118
 DB 1772 CCGGTATCTCATGCGCTCTCTGACAGTGTGGGCCCCCATCTGTCTCATGTTCTTNTCA 1831
 QY 2119 TGTGTTACCTCTTTTGAATCTTGGCATGTGCTTGTGCAAAACATTAATTCGAACACCCAACT 2178
 DB 1832 TGTGCTACATGTTGTCATCTGCGCTGTGCGGTACAGACCCTGCTACGACACCCAACT 1891
 QY 2179 GGAGACCCGATTCGGCTACTACCATTTGGGCGCTTTCTTTTCATGGGAATGATATCTGTC 2238
 DB 1892 GCGTCCACGCTTCAAGTTTACCACTGGACCTCTCTCTCTCTTGGGATGATCTCTGCC 1951
 QY 2239 TGGCTCTGATGTTTCAATTTCTTCTGGTATTATGCAATTTAGCCATGATGATAGTGTGA 2298
 DB 1952 TCGGCTGATGTTTCAATCTGCTCTCTGTTATACGCCNTTTTCGCCATGCTCATTTGCCGCT 2011
 QY 2299 TGATCTCAAGTACATTTGAATACCAAGGAGCTGAGAAAGATGGGGTGTATGGTATCCGCTG 2358
 DB 2012 GCATCTACAAGTACATCGAGTACCGCGGCTGAGAGGAGTGGGGGATGSCATCAGG 2071
 QY 2359 GGTGTCCTCAGTGCAGCGCGTGTGCTTTGCTTTGCTTTCAGTATTGGAGGAAGGACCTCCACACA 2418
 DB 2072 GCCTGTCACTGAATGCTGCCCGCTTACGCCCTGTGCTGTGGTGTGGAAACATGGGCCCCACATA 2131

Qy	2419	CTAAAACTGGAGGCCTCAGTTGCTTGTATTTACTGAAACTAGATGAAGACTTACATGTCA	2478
Db	2132	CCAAGAACTGGAGGCCCCAGGTGTTGTTGATGCTGAACTTGGACTCGGACGAGTGTGTA	2191
Qy	2479	AGCATCTCGCCTCCTCACCTTTGCCCTCAGCTCAAAGCAGGAAAAGTNTCATTATG	2538
Db	2192	AGCACCCCGCCTCTGCTCTCTTCACTCTCAGCTGAAGGCTGGCAAGGGCTGACCATCG	2251
Qy	2539	TGGCTCTGTCATCGTGGGGAACCTTCCTAGAGAACTACGGTGAAGCTTTAGCTGCTGAGC	2598
Db	2252	TGGGATCTGTCTAGAGGGCACTTCTAGACAAGCATGTGGAGGCCCGCAGGCGCTGAAG	2311
Qy	2599	AGACCAATAAGCACCTAATGAGGCGCAGAGAAGGTAAAGAGATTCTGCCAGCTGCTGTGG	2658
Db	2312	AGAATATCCGCTCTCTGATGAGTCAGAGAAGACGAAGGGCTTCTGCCAGCTGTGTGT	2371
Qy	2659	CCGCCAAGCTGAGAGAGGCAATTTCCCACTTCAGTCCAGTCAATGFGGCTTGGGGGCATGA	2718
Db	2372	CCTCCAACTCGAGAGATGGTCCGCTCCCACTGATCCAGTGGCTGGCTCGGTGGCATGA	2431
Qy	2719	AGCACACACGGTGGTATGGCTGGCGCTAATGCTCGCTCAAGCGAAGATGCCCGCG	2778
Db	2432	AACACAACACTGTCTCTATGCGCTTGGCCAGAGGCTTGGAAAGGCGAGATAATCTTTCT	2491
Qy	2779	CTTGGAAAGACTTTTATTTGGCACAGTTCGAGTGAACAATGCTGCCCACTTTTGCACCTGCTGG	2838
Db	2492	CCTGGAGAATTTGTAGACACAGTCGTGNCATCAGCAGCNCATCAGGCCTTGTGG	2551
Qy	2839	TGGCTAAAAACATCTCCTTTTCCCAGCAATGTGAGCAATTTTCTGAGGGCAACATG	2898
Db	2552	TGGCCAAGAACATTGACTTATTTCCACAAAACCAAGAGCGCTTCAGCGACGGGAACATTG	2611
Qy	2899	ATGTGTGGTGAATTTGTGCATGATGGGGGATGCTTTATGCTACTACCAATTTCTACTGAAC	2958
Db	2612	ATGTGTGGTGGATCGTGCATCAGCGGGGCATGCTCATGCTTCTGCCCTTTCTGCTGCGCC	2671
Qy	2959	AGCACAGGTGTGCGAAAGTGCAGCATACGGATCTTCACAGTAGGCCAAATTTAGAAGACA	3018
Db	2672	AGCACAGGTGTGCGGAAAGTGC CGGATGCGCATCTTCATCTGTGGCCAGGTGGATGATA	2731
Qy	3019	ACAGTATCCAAATGAAGAAGCACTAGCCACCTTCTTATATCATCTTACGCAATGAGCGCG	3078
Db	2732	ACAGCATCCAGATGAAGAAGACCTGCAGATGTTTCTGTACCACCTCAGGATCAGTSCCG	2791
Qy	3079	AGGTAGAAGTGGTGAGATGCATCAGCAGTGNATATCAGCATATACATTACAGCGGCATT	3138
Db	2792	AGGTGGAGGTGGTGAGATGTTTGAATAATGATATTTCCGCAATTCACCTATGAGAAGACGC	2851
Qy	3139	TGATGATGGAACAAAGTCCAGATGCTTTGGCACATGCGCTATCAAAACAGAGCGAG	3198
Db	2852	TAATGATGGAGCAGGTGCAGATGCTGAAACAGATGCAATTTGTAAGATGAGCGCGG	2911
Qy	3199	ACAGAGGCGCAATTTGGTGAAGAACCGAAACTCAATCTACGATTGACCAGCATTTGGCT	3258
Db	2912	AGAGAGGCGCCAGCTGATTCTAGCAGAGAACCTGCATCCATCCACACAGCAACTGCTA	2971
Qy	3259	CTGATGAGGACGAGAGACAGAAACCTTATCAGGAGAAGGTGCAATGACTTTGGCAAAAG	3318
Db	2972	GAAACCAAGCCCCCAACA-----CCCGCAAAAGTGCAGATGACATGAGCAGAAAG	3022
Qy	3319	ACAAGTACATGGCATCC---CGGGGACAAAAGCGAGTCAATGGAGGATTTCCAGAGCC	3375
Db	3023	AGAACTCATTTGAGAGAAAACAGGAAACAGGACACTTGGGCCCATCAGGCTTTCAAAGACC	3082
Qy	3376	TGCTTTAATCATGCTCCGACCAAGTCCAAATGTGAGCGCGGATGCATACAGCAGTGAATCTCA	3435
Db	3083	TCTTCAGCCTAAGCCGACCAAGTCCCAAGTCCAGGAGGATGCATCTGCTGTGAAGNTCA	3142
Qy	3436	ACGAGGTTATAGTTAAACAAGTCCCATGAAAGCAAAAGCTGTTTTTATTTGAATATGCCAGGGC	3495
Db	3143	ACGGCGTAGTTTCTCAACAAGTCCCAAGATGCCCACTGGTCTCTGCTGAAATATGCCAGGCC	3202

Qy	3496	CACCCGAAACCTCCTAGGGTGATGAAAACTACATGAGAGTTCCTAGAGGTGCTTACCGAGG	3555
Db	3203	CCCCAAAAGTCGCGACGGGGGACGAGAACTACATGGAGTTCTCTCGAGGTCTCTGACGGAAG	3262
Qy	3556	GACTAGAGCCAGTCCCTACTTGTCCGGGGTGGTGGCAGTGAAGTGATCACCATTTATTTCAT	3615
Db	3263	GGCTGGAACAGGGTCTCTCTGGTCAGGGGTGGTGGCCGAGAAGTCATCACCATCTACTCCT	3322
Qy	3616	AAC 3618	
Db	3323	AAC 3325	
RESULT 14			
XX	AAKS2651		
ID	AAKS2651	standard; cDNA; 5261 BP.	
AC	AAKS2651;		
DT	06-NOV-2001	(first entry)	
XX	Human polynucleotide SEQ ID NO 2180.		
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
XX	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX	Homo sapiens.		
OS	WO200157190-A2.		
XX	09-AUG-2001.		
PD	05-FEB-2001; 2001WO-US04098.		
XX	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0360875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0863561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
XX	Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
PI	WPI; 2001-476283/51.		
XX	P-PSDB; AAM79518.		
DR	Nucleic acids encoding polypeptides with cytokine-like activities,		
PT	useful in diagnosis and gene therapy -		
PT	Claim 1; Page 4544-4545; 6221pp; English.		
XX	The invention relates to polynucleotides (AAKS51456-AAKS53435) and the		
CC	encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: Records for SEQ ID NO 2110 (AAKS52581), 2111 (AAKS52582) and 3666		
CC	(AAM80020) are omitted as the relevant pages from the sequence listing		
CC	were missing at the time of publication.		

XX Sequence 5261 BP; 1019 A; 1626 C; 1567 G; 1049 T; 0 other;
SQ Query Match 33.2%; Score 1414.6; DB 22; Length 5261;
Best Local Similarity 66.8%; Pred. No. 0;
Matches 2103; Conservative 0; Mismatches 1011; Indels 33; Gaps 5;
QY 483 GAGGACATAGAAAGCTCGAATGCTTATCTCAATAATTCATAATTAAGAAGAAGAT 542
DB 150 GATGAAATCCAGAGAAACAGCCATTCCTCAACAATGTGAGGTGGAACAAGAGAGC 209
QY 543 GAATATTTGATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTG 602
DB 210 TTTCTTGAAGGAGNAACATGCGACTTTTCGAGGAGGAGATGACAGTAACCCCATGTG 269
QY 603 TCTTCCCTCCTCAACCGCATGCCAATTAACATTAATCTGACTCAAGGAGCAAAAGAACAT 662
DB 270 TCTCGCTGCTCAACAAGCTGCCAACTACACAACCTGAGCAGGCGGTGTGGAGCAC 329
QY 663 GAGAGGAGAAACATCACTGAAGGGAAGAAAGAGCCACCAAGACCCCAATATGGT 722
DB 330 GAGGAGGAGGAGGAGCGCGCGGGA-----GGCCAAAGGCTCCGCGCATGGC 380
QY 723 ACCTTCATGGGTGTCTACCTCCATGCTTACAAAATATTTTGGAGTGATCCTTTTTTA 782
DB 381 ACCTTCATCGCGCTTACCTGCGCTGCTGAGAAACATCTCGGCGTCACTCTCTCTG 440
QY 783 GCGCTTACATGGGTGGTGGGCAAGCTGGAGTCTTTGAGGCTTTTGCATATGCTCTTATC 842
DB 441 CGCCTGAGCTGATCGTGGGGTGGCTGTGTCTGGAGTCTTCTCATCGTGGCCATG 500
QY 843 TGCTGCTGCTGACAAATGTGATGCTATCTCCATGAGTGCCATTTGCCATTAATGAGTG 902
DB 501 TGCTGCACATGACAAATGTGACCCGCCATTTCCATGAGTGCATCGCTACCAACGCTGTG 560
QY 903 GTGCCAGCTGGGGCTCATCTTTATGATTTCCCGGCACTGGGCGCCAGAGTTGGTGG 962
DB 561 GTCCAGCTGGGGTCTTACTACATGATATCGCGCTCGCTGGGACCCGAGTTGGAGGC 620
QY 963 GCTGTGGCTCTGCTTTTATCTTGGTACCAATTTGACGACGCATGTACATCCTTGGT 1022
DB 621 GCTGTGGCTCTGCTTCTACCTGGGACGACGTTTTCAGGGCCATATATATTTGGGG 680
QY 1023 GCAATGAAATCTTTCTGCTGTATATGTCGCCGAGTGCCATCTTTACAGATGATGAC 1082
DB 681 ACCATCGAGATTTTCTGACGTACATCTCCCGGGTGGCGGCATCTTCAGGCGAGGCT 740
QY 1083 GCACTCAAGGAATACGAGCCATGCTAAATACATGCGGTGCTAGGCGACAGCTTTCTTG 1142
DB 741 CGAGTGGCGAGGCGCGCCCATGCTGCACAAATGCGGTGTGACGGCACGTCACGCTC 800
QY 1143 GTCTTATGATTAAGTGTATTTATCGGCGTACGCTATGTGAACAAGTTTGCCTCANTT 1202
DB 801 GTGCTCATGGCCCTGGTGTCTTCGTGGCGTCAAGTATGTCAACAAGTGGCGTGTGTC 860
QY 1203 TTTCTGGCTGTGTCATGTGTCCATTTTGGCCATCTATGTGGAGCCATCAAGTCTTCT 1262
DB 861 TTTCTGGCTGTGCTGTGTCCATCTCTGGCCATCTATGCGCGGTCAATCAAGTCTGCC 920
QY 1263 TTTGCTCTCCACACTTCCGCTGTGATGCTGGGTAAACCGACCTTTTCATCAAGACAC 1322
DB 921 TTCGACCCCGGACATCCCGGTGTGCTCTGGGGAAACCGCACGCTGTACGGCGCAGC 980
QY 1323 ATTGACGTTTGTCTTAAGACCAAGAAATTAACAACATGACAGTCCCATCAAGTTATGG 1382
DB 981 TTCGATGCTGGCTCAAGGCTTACGGCATCCACAACAACACTCAGCCACCTCCGCGCTCTGG 1040
QY 1383 GGAATCTTGTGTAACGAGTCAATTTTTCATATGCCACCTGTGATGAATCTTTGTTCAC 1442
DB 1041 GGCCTCTTTCGAAACGGTCCCA---GCCACGCGCGCTGTGACGAGTACTTTCATCCAG 1097
QY 1443 AATAAGCTCACTTCAATCCAGGGCATTCCTGATTTGGCTAGTGGTATTAATTAACAGAA 1502

DB 1098 AACAACTGCACGAAATCCAGGGCATCCCGGGCGGGCCAGTGGTGTCTTCTTGAGAAC 1157
QY 1503 CTTTGGAGTAATACCTACCCAAAGGAGAGATCATCGAAAA-----GCTTTACGCC 1553
DB 1158 CTGTGGAGTACGTACGCGACGCGGGCGGTTTGTGGAGAAAGAGTGTGCTCCCTCGGTG 1217
QY 1554 AAATCTTCTGATGCTTTAGGCGAGCTTAAACCATGATATGTTCTTGTGACATCACACC 1613
DB 1218 CCGTGGCAGAGGAGAGCGCGTGCAGCACACTGCGCTACGTGCTCACGACATCGCGGC 1277
QY 1614 TCCCTTACCGCTTCTGGTGGGAATCTCTTTCCTCTGTGTACAGGTATCATGGCTGGATCA 1673
DB 1278 TCCCTTACCTGCTGGTGGCATCTACTTCTCTCCGTGACCGGTATCATGGCGGTTCAT 1337
QY 1674 AACAGATCTGAGATCTGAAAGATGCTCAGAAAGTCTATTCCGATTTGTTACTATCTTGC 1733
DB 1338 AACCGGTCCGGGACCTCAAGGATGCACAGAAGTCCATCCCAAGGGGACCATCTCTGGCC 1397
QY 1734 ATCTGACCACTCTTCTTGTATTTAAGCAATGTTGCTCTTCTTGTGGTGTGATTTGAA 1793
DB 1398 ATAGTGACGAGCTCTTTCATCTCTCTCTGCAATGTGCTGTTGGGCGCTGCAATTGAA 1457
QY 1794 GGGGTGTTCTCAGAGCAAGTTCGGTGATGCTGTGAAAGGTAAATTTGGTGTAGGCACC 1853
DB 1458 GCGTGGTCTTACAGATAAGTTCGGGAGGCGCTGACAGGGAACTTGGTCTATCGGCATG 1517
QY 1854 TTATCTTGGCCATCCCATGGGTGATTTATTTGGTCTCTTCTTTTCAACATTTGGGCT 1913
DB 1518 CTGGCTGGCCCTCCCGCTGGTCTATGTCATCGCTCTCTCTCTCTCACCTGGCTGGC 1577
QY 1914 GGACTTCAGAGCTTCACAGGTGCACGAGGTGCTCAAGTCTATTGCCAAGGATTAACATC 1973
DB 1578 GGCCTGCAGACCTTCAGGGGCGACCGCGCTACTGCAGGGCATTTGCCCTGTCAGCGCATC 1637
QY 1974 ATACGTTCTGAGGGTTTTTGGCCACAGCAAGCAACAAAGCACTACCTGGGCTTTTA 2033
DB 1638 GTCCCTTCTCTGAGGTGTTTTGGCCACAGGAAAGCAACGGGAGCCACAGTGGCGGTG 1697
QY 2034 CTTCTAACTGCTGCATTTGACAGCTTGGAACTCATTTGCTCTCTCTGGATCTTTGTGGCC 2093
DB 1698 CTGCTGACAGTCTCTCATCTGGAGACTGGCATCTCTCATCGCTCTCTGACAGCGTGGCC 1757
QY 2094 CCAATCTTTCCATGTTTTTCTCATGTGTTTACCTCTTTGTAACTTTGGCATTTGCCCTG 2153
DB 1758 CCGATCTCTCCATGTTCTTCTCATGTGCTACCTGTTGTTGTAACCTGGCTGCGCGGTG 1817
QY 2154 CAACATTTACTTCCAAACCACTGGAGACCCCGATTCGCTACTACCATTTGGGCGCTT 2213
DB 1818 CAGACCTGCTACGTACCCCACTGGCGTCCACGCTTCAAGTTCTACACTGGACCTG 1877
QY 2214 TCTTTTCATGGGAATGAGTATCTGTGCTGCTGATGTTTCATTTCTTCTGGTATTATGCC 2273
DB 1878 TCCCTTCTGGGTATGAGCTGTGCTGGCGTGTATGTTTCATCTGCTCTGGTACTACGG 1937
QY 2274 ATTGTAGCATGTAATAGCTGGTATGATCTCAAGTACATTTGAATACAAAGGAGCTGAG 2333
DB 1938 CTGTCCGCGCATGCTATCGCTGGTGTGATCTTCAAGTACATCGAGTACCGGCGGCGCAG 1997
QY 2334 AAAGATTTGGGTGATGTTATCCGTTGGGTGTCCTCTCAGTGCAGCCGCGTGTCTTGTGCTT 2393
DB 1998 AAGGATTTGGGCGATGAGCATCCGTGGCTATTCCTCTGAACCGCGCGCTGACGCCCTGCTG 2057
QY 2394 CGATTGGAGGAAGGACCTCCACACACTAAAGCTGGAGGCTCAGTTGCTTGTATTACTG 2453
DB 2058 GCGTGGAGCAGCTTCCCGCCACACCAAGAACTGGAGGCCCCAGGTGCTGTGTATGCTG 2117
QY 2454 AAACTAGATGAAGACTTACATGTCAAGCATCTCGCTCTCTCACTTTTGTCTCAAGCTC 2513
DB 2118 AACCTGACGCGGAGCAGGCGCATGAAGCACCCCGCGCTGCTGTCTTCTCACGCTCGCAGCTG 2177
QY 2514 AAAGCAGGAAGAGTNTCACTATTTGTGGGTCTGTCTCATCTGGGGGAACTTCTTAGAGAAC 2573
DB 2178 AAGCCCGCAAGGGCCTGACCATCTGGGTCTGGTGTGGAGGGGACGTACCTGGACAA 2237

QY 2574 TACGGTGAAGCTTTAGCTGCTGAGCAGACCAATAAGACACCTAATGAGGCGACAGAGAAGTA 2633
Db |||||
QY 2238 CACATGAGGCTCAGCGGCCGAGGAGAACATACGGTCCCTAATGAGCAGACAGAGAAGACC 2297
Db |||||
QY 2634 AAAGAGTTCTGCGAGTGTGTGGCGCGCAAGCTGAGAGAGGGGATTTCCACCTCATC 2693
Db |||||
QY 2298 AAGGGCTTCTGCGAGTGTGTGCTCGTCCAGCTCGGGATGGCATGTCCACCTGTATC 2357
Db |||||
QY 2694 CAGTCATGTGGCTTGGGGGCGATGAGCACACAGCTGGTGTGATGGCTGGCTAATGGC 2753
Db |||||
QY 2358 CAGTCGGCGGCTTGGCGGCGCTGAAGCACACACGGTCTCATGCGCTGGCCGCGATCC 2417
Db |||||
QY 2754 TGGCGCTCAAGGCAAGATCCCGCGCTTGGAAAGACTTTTATTTGGCACAGCTTTCAGATGACA 2813
Db |||||
QY 2418 TGAAGCAGGAGACAAACCCCTTCTCTGGAAGACTTTGTAGACACCGTCCGCGACACC 2477
Db |||||
QY 2814 ACTGTGCCCATTTTGCACTGTGTGGCTAAACATCTCTCTTTCCAGCAATGTG 2873
Db |||||
QY 2478 ACCGCGCGCACAGGCTCTGTGTGGCGCAAGACGTCGACTCGTTTCCGCAAAACACAG 2537
Db |||||
QY 2874 GAGCAATTTCTGAGGGCAACATTGATGTGTGGTGTGATGTGCATGTGGGGGATGCTT 2933
Db |||||
QY 2538 GAGCGCTTGGCGGGGGCGCACATCGACGTGTGGTGTGATGTGCACGCGCGGATGCTC 2597
Db |||||
QY 2934 ATGCTACTACCATTTCTACTGAAACAGACCAAGGTGTGGCGAAAGTGCGAGCATACGGATC 2993
Db |||||
QY 2598 ATGTGCTGCCCTTCTCTGCTGGCGCAGCACAGGTGTGGAGNAGTGCCGGATGCTATC 2657
Db |||||
QY 2994 TTCACAGTACCCAAATTGAAGACAAACAGTATCCAAATGAAGAGACCTTACGCCCTTC 3053
Db |||||
QY 2658 TTCACGCTGCCCGAGGTGACGACAAACAGCATCCAGATGAAGAGGACCTGCGAGATGTT 2717
Db |||||
QY 3054 CTATATCACTTACGCAATGAGCGGAGGTAGAGTGTGGAGATGCATCACAGTATATA 3113
Db |||||
QY 2718 TTGTACCACTTGGCATCAGCGCGGAGGTGGAGTGTGGAGATGGTTGAAAACACACATA 2777
Db |||||
QY 3114 TCAGCATATCTTACGAGCGCACTTTGATGATGGAAACAAAGTCCAGATGCTTGGGCAC 3173
Db |||||
QY 2778 TCTGCTTTCCCTACGAGGAGCACTAATGATGGAGCAGAGTTCGAGATGCTGAAGCAG 2837
Db |||||
QY 3174 ATGCGGCTATCCAAACAGAGCGAGACAGAGAGGCAAAATTTGGTGAAGAACCGCAACTCA 3233
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XX
AC AAI59217;
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DT 22-OCT-2001 (first entry)
XX
Human polynucleotide SEQ ID NO 1420.
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DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokineic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO20015312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
XX
DR P-PSDB; AAM40061.
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 1420; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
SQ Sequence 3711 BP; 769 A; 1039 C; 1124 G; 779 T; 0 other;

Query Match 32.8%; Score 1395.4; DB 22; Length 3711;

Best Local Similarity 69.7%; Pred No. 0;

Matches 1920; Conservative 0; Mismatches 818; Indels 15; Gaps 2;

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Job time : 1048 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 17:51:45 ; Search time 1219 Seconds
(without alignments)
11513.847 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2862.6	67.2	6075	11	US-09-835-976B-5
5	2732.2	64.1	6052	11	US-09-835-976B-9
6	1674	39.3	3726	10	US-09-917-800A-1667
7	1418	33.3	5239	11	US-09-835-976B-1
8	1415	33.2	5155	11	US-09-835-976B-13
9	1392.4	32.7	5907	11	US-09-835-976B-11
10	735	17.3	807	11	US-09-835-976B-110
11	613.4	14.4	2290	11	US-09-835-976B-112
12	446.4	10.5	478	11	US-09-918-995-9696
13	434	10.2	489	11	US-09-835-976B-84
14	262	6.2	1014	11	US-09-835-976B-18
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Db	1501	ATCTTTGGAGTAATTACCTACCCAAAGGAGAGATCATCGAAAAAGCCTTACGCCAAATCTT	1561
Qy	1561	CTGATGCTTAGGCAAGCTTAAACCATGAATATGTTCTTGTGTGATCATCACACCTCCTTCA	1621
Db	1561	CTGATGCTTAGGCAAGCTTAAACCATGAATATGTTCTTGTGTGATCATCACACCTCCTTCA	1621
Qy	1621	CGCTTCTGGTGGGAATCTCTTTCCCTCTGTATACAGGTATCATGGCTGGATCAAAACAGAT	1681
Db	1621	CGCTTCTGGTGGGAATCTCTTTCCCTCTGTATACAGGTATCATGGCTGGATCAAAACAGAT	1681
Qy	1681	CTGGAGATCTGAAGAATGCTCAGAAGTCTATTCCGATTGGTACTATCCTTTGCCATCTCTGA	1741
Db	1681	CTGGAGATCTGAAGAATGCTCAGAAGTCTATTCCGATTGGTACTATCCTTTGCCATCTCTGA	1741
Qy	1741	CCACCTCCTTTGTTTATTAAAGCAATGTTGTCCTTTTGGTGCATGTTATTGAAGGGGTG	1801
Db	1741	CCACCTCCTTTGTTTATTAAAGCAATGTTGTCCTTTTGGTGCATGTTATTGAAGGGGTG	1801
Qy	1801	TTCTCAGAGACAAGTTCGGTGATGCTGTGAAGATTAATTTGGTGGTAGGCACCTTATCTT	1861
Db	1801	TTCTCAGAGACAAGTTCGGTGATGCTGTGAAGATTAATTTGGTGGTAGGCACCTTATCTT	1861
Qy	1861	GGCCATCCCCATGGGTGATTGTTATTGGCTCCTTTTCAACATGTGGGGCTGGACTTC	1921
Db	1861	GGCCATCCCCATGGGTGATTGTTATTGGCTCCTTTTCAACATGTGGGGCTGGACTTC	1921
Qy	1921	AGAGCTCAGAGGTGCAACCGAGGCTGCTACAGCTATTGGCAGGATAACATCATACCGT	1981
Db	1921	AGAGCTCAGAGGTGCAACCGAGGCTGCTACAGCTATTGGCAGGATAACATCATACCGT	1981
Qy	1981	TTCTGAGGGTTTTTGGCCACAGCAAAAGCAATGGGAACCTTACCTGGGCTTTTACTTCTAA	2041
Db	1981	TTCTGAGGGTTTTTGGCCACAGCAAAAGCAATGGGAACCTTACCTGGGCTTTTACTTCTAA	2041
Qy	2041	CTGCTGCCATTGCAGAGCTTGGAACTACTCATTTGCCCTCCCTGGATCTTTGTGGCCCCAATTC	2101
Db	2041	CTGCTGCCATTGCAGAGCTTGGAACTACTCATTTGCCCTCCCTGGATCTTTGTGGCCCCAATTC	2101
Qy	2101	TTTCCATGTTTTTTCTCATGTGTACCTCTTTGTAAACCTTGGCATGTGCCTTGCACACAT	2161
Db	2101	TTTCCATGTTTTTTCTCATGTGTACCTCTTTGTAAACCTTGGCATGTGCCTTGCACACAT	2161

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DB 2161 TACTTCGAACACCCAACTGGAGACCCCGATTCCGCTACTACCATTTGGGGCCCTTTCTTTCA 2220
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DB 2221 TGGGAATGAGTATCTGTCTGGGCTCTGATGTTTCTTCTGTTATTTATGCAATTTGTAG 2280
QY 2281 CCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGGAGCTGAGAAGAAT 2340
DB 2281 CCATGGTAATAGCTGGTATGATCTACAAGTACATTTGAATACCAAGGAGCTGAGAAGAAT 2340
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QY 2941 TACCATTCTTACTGAAACAGCAGCAGGTGTGGGAAAGTGCAGATCCGATCTTCACAG 3000
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QY 3181 TATCCAAAACAGAGCGAGACAGAGGCGCAATTTGGTGAAGACCGAACTCAATGCTTAC 3240
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RESULT 2

US-09-835-976B-3

; Sequence 3, Application US/09835976B

; Publication No. US20030027983A1

GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4215
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (165)..(3569)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (267)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1578)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3387)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
US-09-835-976B-3

Query Match 97.2%; Score 4139.4; DB 11; Length 4215;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 4208; Conservative 0; Mismatches 5; Indels 47; Gaps 2;
QY 1 TGAGTAAAGTATCTTAGTGGGCTTTTGTGGTGTGAATCAAGGTATTGAAATG 60
DB 1 TGAGTAAAGTATCTTAGTGGGCTTTTGTGGTGTGAATCAAGGTATTGAAATG 60
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DB 61 TGTATTTTCAAGTTATCTTTGTATTCAGTCAAAAGTAGCTAGCGTAAGAGGAAGAT 120
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DB 421 AGGATGTCATCGAG-----G 435
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DB 436 ACACCGGACATAGAAGCTCGAAATGCTTATCTCAATTAATTCCAATTATGAAGAAGGAG 495

QY 541 ATGAATATTTTGTATAAAATTTGGCACTCTTTGAGGAAGAAATGGACACCGAGACCGAAGG 600
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QY 601 TGTCTTCCCTCTCAACCGCATGGCCATTAACACTAATCTCACTCAAGGACGAAGGAAC 660
DB 556 TGTCTTCCCTCTCAACCGCATGGCCATTAACACTAATCTCACTCAAGGACGAAGGAAC 615
QY 661 ATGAAGAGGACAGAAAACATCACTGAAGGGAAGAAAGACCCACCAAGACCCCCCAAAATGG 720
DB 616 ATGAAGAGGACAGAAAACATCACTGAAGGGAAGAAAGACCCACCAAGACCCCCCAAAATGG 675
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QY 841 TCTGCTGCTGTACAAATGTTGACTGTCTCTCATGAGTGCCATTCGCCACTAATGGAG 900
DB 796 TCTGCTGCTGTACAAATGTTGACTGTCTCTCATGAGTGCCATTCGCCACTAATGGAG 855
QY 901 TGGTCCAGCTGGGGGCTCATACTTTATGATTTCCCGGGCACTGGGGCCAGAGTTTGGTG 960
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DB 1216 CTTTTGCTCTCCACACATTCGCGGTCTGCATGCTGGGTAAACCGCACTCTTTTCATCAAGAC 1275
QY 1321 ACATTTGAGTTTGTCTTAAGACCAAGGAAATTAACAAATGACAGTCCCATCAAGATTAT 1380
DB 1276 ACATTTGAGTTTGTCTTAAGACCAAGGAAATTAACAAATGACAGTCCCATCAAGATTAT 1335
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QY 1501 ATCTTTGAGTAAATTAACCTACCCAAAGGAGAGATCATGAAAGGCTTCAGGCAAAATCTT 1560
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DB 1636 CTGGAGATCTGAAGATGCTCAGAAAGTCTATTCCGATTGGTACTATCTTTCGCATCCTGA 1695
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DB 1696 CCACCTCTCTTTGTTTATTAAAGCAATGTTGCTCTTTTGGTGATGATATTGAAGGGTTG 1755
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DB 1756 TTCTCAGAGACAAGTTCGGTGATGCTGCAAGAGTAAATTTGGTGATGAGCACTTATCTT 1815
QY 1861 GGCCATCCCCATGGGTGATTGTTATTGGCTCTCTTTTCAACATGTGGGGCTGCACTTC 1920
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QY 1921 AGAGCCTCACAGGTGCACCGAGGTGCTACAAGCTATTGGCCAAAGGATAACATCATACCGT 1980
DB 1876 AGAGCCTCACAGGTGCACCGAGGTGCTACAAGCTATTGGCCAAAGGATAACATCATACCGT 1935
QY 1981 TTCTCAGGGTTTTTGGCCACACAGAAAGCCAAATGGGGAACTTACCTGGGCTTTACTTTCTAA 2040
DB 1936 TTCTCAGGGTTTTTGGCCACACAGAAAGCCAAATGGGGAACTTACCTGGGCTTTACTTTCTAA 1995
QY 2041 CTGCTGCCATTGCAGAGCTTGAATACTCATTTGCCCTCCCTGGATCTTGTGGCCCAATTC 2100
DB 1996 CTGCTGCCATTGCAGAGCTTGAATACTCATTTGCCCTCCCTGGATCTTGTGGCCCAATTC 2055
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DB 2056 TTTCATGTTTTTCTCATGTGTTTACCTCTTTGTAACTTGGCATGTGCTTTGSCAAACAT 2115
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QY 2221 TGGGAATGAGTATCTGTCTGGCTCTGATGTTCAATTTCTCTGGTATTATGCAATTTAG 2280
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QY 3601 TCACCATTTATTCATAACCTACTCTGAATGACCGTGTGACCTGTTTTCTTTAAAGGCC 3660
DB 3556 TCACCATTTATTCATAACCTACTCTGAATGACCGTGTGACCTGTTTTCTTTAAAGGCC 3615
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QY 3901 GCCAATAAATGAATTTGGTAAAAAGGATGCTAGAAAATTCAACTGAAGAAAAAAGCAAGTC 3960
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Db 4094 CACTGCTGTAATTTTATATTAGATATCTAACTTGAACATGCTGAGCCTCTACTTTCTT 4153
QY 4201 CAAAAACATCCCCCAAAATACAGATTTAAATATCCAAAAAAGAAAAAAGAAAAA 4260
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RESULT 3

US-09-835-976B-7
; Sequence 7, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 6120
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3453)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (106)
; OTHER INFORMATION: n-c or a, Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (925)
; OTHER INFORMATION: n-c or a, Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2545)
; OTHER INFORMATION: n-c or a, Xaa-Leu or Ile

US-09-835-976B-7
Query Match 69.5%; Score 2958.8; DB 11; Length 6120;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 3365; Conservative 0; Mismatches 436; Indels 76; Gaps 7;

QY 162 AAAATGCAATCTCTCCAGAAACCAACCAAGATGGCTTCAGTTCGGTTCATGTTGACACGG 221
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QY 222 ACAAGATCGATGACATTTCCAGGTTTGTCCAGACACAGTCCGGACNTCAGCTCTCGATCT 281
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QY 282 AGTTCGCCAGTAAGATTTAGCTCCCGGAAAGCGTCCCTGAAACAAAGCCGAGTGAAGCCT 341
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QY 462 GAACACGCAACTCTGTAGACGCGGACATAGAAAGCTCGAAATGCTTATCTCAATAAT 521
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QY 882 GCCATTGGCCTAATGGAGTGGTGGCAGCTGGGGCTCATACTTTATGATTTTCCCGGCA 941
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QY 1002 GCAGCCATGTACATCTTGGTGGCCTTGAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1061
Db 841 GCAGCCATGTATATTCTTGGTGGCCTTGAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 1062 GCCATCTTTTACAGTGAAGCAGCTCAAGGAATCAGCAGCCATGCTAAATAAACATGCGT 1121
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3538 ACTC-----TATTCTTGACAGCTGAGCCCC 3563
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3789 TCAGGACGATTTTCAAGACACCGGTGAGTGAC 3825
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RESULT 4
US-09-835-976B-5
; Sequence 5, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6075
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS (3408)
; LOCATION: (4)..(3408)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (307)
; OTHER INFORMATION: n-c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1894)
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; OTHER INFORMATION: n-c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3340)
; OTHER INFORMATION: n-c or a, Xaa=Leu or Ile
US-09-835-976B-5
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Query Match 67.2%; Score 2862.6; DB 11; Length 6075;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 435; Indels 121; Gaps 8;

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QY 222 ACAAGATCGATGACATTTCCAGGTTTGTGCACACACAGTCCGGACNTCAGCTCTCGATCT 281
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QY 61 ACTAAGATGTAGTACATTTCCAGGTTTGTGCACACACAGCCCGGACCTCAGCTCTCGGCT 120
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QY 642 ACTCAAGGAGCAAGGAAACATGAAGGACGAGAAACATCACTGAAGGGAAGAAAGAGCC 701
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1876 GATCTGTTGGCCCCAATTTTCCATGTTTTTCTCATGTGTTACTCTTTGTGAACTTG 1935
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RESULT 5

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US-09-835-976B-9
; Sequence 9, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6052
; TYPE: DNA
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; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)..(3385)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (284)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
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; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3008)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; US-09-835-976B-9

Query Match 64.1%; Score 2732.2; DB 11; Length 6052;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 3120; Conservative 0; Mismatches 408; Indels 76; Gaps 7;

QY 435 GACCTGAGTCAGAACTCCATCACAGGGGAAACACAGCCCACTGTTAGACGACCGACATAG 494
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Db 266 AAAGCCCGAAATGCTTATNTCAATAATTCCAATATTAAGAGAGGAGACGAATATTTGAT 325
QY 555 AAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTGTCTTCCTCCTC 614
Db 326 AAAAATTTGGCACTCTTTGAGGAAGAAATGGACACAGACCGAAGGTGTCTTCCTCCTC 385
QY 615 AACCCGATGGCCAAATTAACACTAATCTGACTCAAGGAGCAAGGAACATGAAGAGGAGAA 674
Db 386 AACCCGATGGCCAACTATACAAATCTGACACAAAGGAGCAAAAGAAACATGAAGAGGAG 445
QY 675 AACATCACTGAAGGGAAGAAAGAGCCACCAAGAGCCCCCAATGGGTACCTTCATGGGT 734
Db 446 AACATCACTGAAGGGAAGAAAGAGCTTACCAAGAGCCCCCAATGGGTACCTTCATGGGT 505
QY 735 GTCTACCTCCCATGCTCTACAAATAATTTTGGAGTGATCCTTTTTTACGCCCTTACATGG 794
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QY 2295 GGTATGATCAAGTATCAATTAATCAAGGCTGAGAAAGATGGGTGATGATGATC 2354
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Qy 4011 TGAC 4014
Db 3754 GCAC 3757

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US-09-917-800A-1667
; Sequence 1667, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIORITY FILING DATE: 2001-07-31
; PRIORITY APPLICATION NUMBER: US 60/222,040
; PRIORITY FILING DATE: 2000-07-31
; PRIORITY APPLICATION NUMBER: US 60/222,880
; PRIORITY FILING DATE: 2000-11-02
; PRIORITY APPLICATION NUMBER: US 60/290,029
; PRIORITY FILING DATE: 2001-05-11
; PRIORITY APPLICATION NUMBER: US 60/290,645
; PRIORITY FILING DATE: 2001-05-15
; PRIORITY APPLICATION NUMBER: US 60/292,336
; PRIORITY FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1667
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; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_0192229
US-09-917-800A-1667

Query Match 39.3%; Score 1674; DB 10; Length 3726;
Best Local Similarity 71.6%; Pred. No. 0;
Matches 2212; Conservative 0; Mismatches 872; Indels 6; Gaps 1;

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1971 TGAAGAGAGTGGGTGTGGATTCGAGGCTGTCTCTGTAGTGGCGGACAGATATGCAT 2030

2390 GCTTCGATTGGAGGAGCCTCCACACACTAAATAACTGGAGGCTCAGTTGCTTGTATT 2449
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2990 GATCTTACAGTACGCCAATTTAGAAAGCAACAGTATCCAAATGAAGAGGACCTAGCCAC 3049
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3410 GCGGATGCATACAGCAGTGAACCTCAACGAGGTTTATAGTTAAACAAGTCCCATGAAGCAA 3469
3051 GCGTATGCACACTCTGTGAAGCTCAATGAAGTCAATTTGTACACGCTCCCATGATGCCG 3110
3470 GCTGGTTTTATTGAATATGCGAGGCGCACCCCGGAAACCTGTGAGGGTGTGATGAATACTACAT 3529

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Db 3111 CCTGTCTTACTGAACATGCCCGGCCCTTAAGAACAGTGAAGGTGATGAACTACAT 3170
Qy 3530 GGAGTTCTTAGAGTCTTACCGAGGAGTACGAGGAGTCCCTACTTGTCCGGGGTGGTGG 3589
Db 3171 GGAAATTCCTTTGAAGTCCCTAACCGAGGCGCTTGAACGGGGTGTGTTGGTGGTGGTGG 3230
Qy 3590 CAGTGAAGTGATCACCATTATTTATCAACC 3619
Db 3231 CCGGGAAGTCATCACCATCTATCTTGAGC 3260

RESULT 7
US-09-835-976B-1
; Sequence 1, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)..(3253)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (161)
; OTHER INFORMATION: n=a or c, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (260)
; OTHER INFORMATION: n=a or t, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3086)
; OTHER INFORMATION: n=a or c, Xaa=Leu or Ile
US-09-835-976B-1

Query Match 33.3%; Score 1418; DB 11; Length 5239;
Best Local Similarity 66.9%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 1010; Indels 33; Gaps 5;

Qy 483 GACGGACATAAGAAAGCTCGAAATGCTTATCTCAATAATTCCAATTATGAAGAAGGAGAT 542
Db 131 GATGAAATCCAAAGAGAAACAGCCATTCTNTCAACAATGTCGAGGTGGAACAAGAGAGC 190
Qy 543 GAATATTTGATAAATAATTGGCACTTTTGAGGAAGAAATGGAACACGACCGAAGGTG 602
Db 191 TTTCTTTGAAGGGGAAGAACATGGCACTTTTCGAGGAGGAGATGGACAGTAACCCCATGGTG 250
Qy 603 TCTTCCTCTCTCAACCGCATGGCAATTACATTAATCTGACTCAAGGAGCAAGGAACAT 662
Db 251 TCTCTGCTGNTCAAGAAGTGGCCAACTACCAACCTGAGCCAGGGCGTGGTGAGCAC 310
Qy 663 GAAGAGCGCAAAACATCTAGAGGGAAGAAAGAGCCCAAGAGCCCAAGAGTGGT 722
Db 311 GAGGAGGACGAGGAGAGCGCGGGCGGGA-----GGCCAAAGGCTCGGCGCATGGGC 361
Qy 723 ACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCTCTTTT 782
Db 362 ACCTTCATGGGTGTCTACCTCCCATGTCTACAAAATATTTTGGAGTGATCTCTTT 421
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Qy 783 GCCTTACATGGGTGGTGGGCACAGCTGGAGTCTTCTCAGGCTTTTTCGAATTTGCTCCTTATC 842
Db 422 CGCTGAGCTGATCGTGGGGGTGGCTGGTGTCTTGGAGTCTTCTCCTCATCGTGGCCATG 481
Qy 843 TGCTGCTGCTGTAACAATGTTGACTGCTATCTCCATGAGTGCATTCGACCACTAATGAGTG 902
Db 482 TGCTGCACATGTACAATGCTGACCGCCATTTCCATGAGTGCATCGCTACCAACGCTGTG 541
Qy 903 GTGCCAGCTGGGGCTCATACTTTATGATTTCCGGGCACCTGGGGCCAGAGTTTGGTGGG 962
Db 542 GTCCAGCTGGGGGTCTCTACTACATGATATCGCGCTCGCTGGGACCGAGTTTGGAGGC 601
Qy 963 GCTGTTGGCTCTGCTTTTATCTTGGTACCAACATTTTGACAGAGCCATGTATCATCTTGGT 1022
Db 602 GCTGTGCGCTCTGCTTCTACTTGGCACAGAGTTTGACGGGCCATGTATATTTTGGGG 661
Qy 1023 GCCATTGAAATCTTTCTGGTCTATATGTCGCCGAGTGCATTTTTCACAGTATGAC 1082
Db 662 ACCATCGAGATTTTCTGACGTACATCTCCCGGTGGCGCATCTTCAGCGCGAGGCT 721
Qy 1083 GCATCAAGGAATCAGAGCCATGCTAAATAAACATCGGTGCTAGCGGCACAGCTTTCTTG 1142
Db 722 GCAGTGGCGAGCGCGCCCATGCTGCACAAACATGCTGTGACGGCACGTGCACGCTC 781
Qy 1143 GTCTCTTATGTTAGTGGTATTTATCGCGCTACGCTATGTGAACAAAGTTTGCCTCAN 1202
Db 782 GTGCTCATGGCCCTGGTGTCTTCTGGGCGTCAAGTATGTCAACAAGCTGGCGTGTG 841
Qy 1203 TTCTGCGCTGTGTCATTTGTCATCTTGGCCATCTATGTGGAGCATCAAGTCTTCT 1262
Db 842 TTCTGCGCTGCTGCTGCTGCTCATCTGCGCCATCTATGCGCGCTCATCAAGTCTGCC 901
Qy 1263 TTTGCTCTCCACACTTCCCGGTCTGCATGCTGGGTACCGGCACCTTTTCATCAAGACAC 1322
Db 902 TTCGACCCCCCGGACATCCCGGTCTGCGCTCTGGGGAACCGCACGCTGTACGGCGCAGC 961
Qy 1323 ATTGACGTTTGTCTTAAGACCAAGAAATTAACAACATGACAGTCCCATCAAAAGTTATGG 1382
Db 962 TTCGATGCTGGTCAAGGCTTACGGCATCCACAACACTCAGCCACCTCCGCGCTCTGG 1021
Qy 1383 GGATTTCTGTAACTCGAGTCAATTTTTCATGCTGAGTGAATATCTTTGTCATC 1442
Db 1022 GGCCTCTTCTGCAACGGCTCCCA---GCCACAGCGCGCTGTGACGAGTACTTTCATCCAG 1078
Qy 1443 AATACGTCACCTCAATCCAGGCAATCTCGATTGGCTAGTGGTATTAATACAGAGAT 1502
Db 1079 AACACGTCACCGAAATCCAGGCAATCCGGGCAATCCGGGCGCGGCGAGTGTCTTCTCGAGAAC 1138
Qy 1503 CTTTGGAGTAATTACCTACCAAGGAGAGATCATCGAAAA-----GCCTTCAGCC 1553
Db 1139 CTGTGGAGTACGTACGCCACCGCGGGCGTGTGGGAGAGAAAGTGTGCCCTCGGTG 1198
Qy 1554 AATCTTCTGATGCTTAGGAGCTTAAACCATGAATATGTTCCTTTGTAACATCACCACC 1613
Db 1199 CCGGTGGCAGAGGAGAGCGCTGCCACACACTGCGCTACGTCTCACGACATCGCGGC 1258
Qy 1614 TCCCTACGCTTCTGGTGGAACTCTTCTTCCCTGTTACAGGTATCATGGCTGATCA 1673
Db 1259 TCCCTTACCCCTGCTGGTTGGCATCTACTTCCCTCCGTCGCGGTATCATGGCGGTTCA 1318
Qy 1674 AACAGATCTGAGATCTGAAAGATGCTCAGAAAGTCTATTTCGATTTGGTACTATCTTGGC 1733
Db 1319 AACCGTCCGGGACCTCAAGGATGCACAGAAAGTCCATCCCAACCGGACCATCTCTGGCC 1378
Qy 1734 ATCTGACACACTCTCTTTGTTTATTAAGCAATGTTGTCTCTTTTGGTGCATGATGAA 1793
Db 1379 ATAGTGACGAGCTCTTTCATCTATCTCTCTGCAATTTGCTGCTTTGGGCGCTGCATGAA 1438
Qy 1794 GGGGTGTTCTCAGAGACAAGTTCGGTATGCTGTGAAGGTAAATTTTGGTGTAGGCACC 1853
Db 1439 GCGGTGCTTACGAGATAAGTTTCGGGAGGCGCTTCAGGGGAACCTGCTCATCGCATG 1498
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1854 QY TTATCTTGGCCATCCCATGGGTGATTGTTATTGGCTCCTTCTTTTCAACATGTGGGCT 1913
1499 Db CTGGCTGGCCCTCCCTCTGGGTGATCGTCATCGGCTCTTCTTCTCACCTCGGGTGC 1558
1914 QY GGACTTCAGAGCTCAACAGTGCACCGAGGCTGCTACAAGCTATTGGCCAAGGATAACATC 1973
1559 Db GGCTTCAGAGCTCAACAGTGCACCGAGGCTGCTACAAGCTATTGGCCAAGGATAACATC 1618
1974 QY ATACCGTTTCTGAGGTTTCTGGCCACAGCAACCAATGGGGAACCTTACCTTGGGCTTTA 2033
1619 Db GTCCCTCTCTGAGGTGTTTGGCCACGGGAAGGCCAACGGGAGGCCCACTGGGCGCTG 1678
2034 QY CTTCTAACTGCTGCCATTGCAGAGCTTGGAAATACCTATTGCTCCTCCTGATCTTGTGGCC 2093
1679 Db CTGCTGACAGTCTCTCATCTGCAGAGCTGCACTCTCATCGCTCTCTGGAAGCGTGGCC 1738
2094 QY CCAATCTTTTCATGTTTCTCATGTTTACCTCTTTTGAATCTTGGCATGTGCTTTG 2153
1739 Db CCGATCTCTCCATGTTCTTCTCATGTTTACCTGTTCTGTAACCTGCTGCAACCTGGCCCTG 1798
2154 QY CAAACATTACTTGAACCCCACTGGAGACCCGATTCGGCTACTACCATTTGGGCGCTT 2213
1799 Db CAGACCTCTACTGTAACCCCACTGGCGTCCACGCTTCAAGTTCTTACCCTGGAACCTCTG 1858
2214 QY TCTTTTCATGGGAATGAGTATCTGCTGGCTCTGATGTTTCATTTCTTCTGTTATTATGCC 2273
1859 Db TCTTTTCTGGGTATGAGCTGTGCTGGCGCTGATGTTTCATCTGCTCTGGTACTACGCG 1918
2274 QY ATTGTAGCCATGTTAATAGCTGGTATGATCTCAAGTACATTGAAATACCAAGGAGCTGAG 2333
1919 Db CTGTCGGCATGCTCATGCTGGCTGATCTCAAGTACATGAGTACCGCGGGGCGGAG 1978
2334 QY AAAGAAATGGGGTATGGTATCGTGGCTGCTCCTCAGTGCAGCGCGGTTCCTTTGCTT 2393
1979 Db AAGGAGTGGGGGATGGCATCGTGGCTTATCCCTGAACCGCGCGCTACGCTCCCTGCTG 2038
2394 QY CGATTGGAGGAGGACTTCCACACTAAACTGAGGCGCTCAGTGTCTGTGTTATTACTG 2453
2039 Db CCGCTGGAGACGCTCCCCCACCACCAAGAACTGGAGCCCCAGGTGCTGTGTGATGCTG 2098
2454 QY AAATAGATGAGACTTACATGTCAAGCATCTCGCCTCTCACCTTTGCTCTCACAGCTC 2513
2099 Db AACCTGGAGCGGAGCGCGTGAAGCACCCCGCTGCTGTCTTCAAGTGGAGCTG 2158
2514 QY AAAGCAGGAAGGTTNCTATTTGTGGCTCTGTATCGTGGGAACTTCTTAGAGAAC 2573
2159 Db AAGCGCGGAGGGCTGACCATCTGCGGCTCGGTGCTGGAGGGGACGTACTCTGACAAG 2218
2574 QY TACGGTGAAGCTTTAGCTGCTGAGCAGACCAATAAAGCACTTAATGGAGCGAGAGGTA 2633
2219 Db CATATGAGGCTCAGCGGCGCGAGAGAACATACCGTCTCTTAATGAGCAGAGAGAGACC 2278
2634 QY AAAGATTCTTGCAGCTGTGTGGCGCGCAAGCTGAGAGGGGCAATTTCCACCTCATC 2693
2279 Db AAGGGCTTCTGCCAGCTGTGTCTGCTCCAGCTGCGGATGGCATGTCCACCTGATC 2338
2694 QY CAGTCATGTGGCTTTGGGGCATGAAGCACACACGGTGGTGAATGGGCTGGCTTAATGGC 2753
2339 Db CAGTGGCGGGCTGGCGGGCTGAAGCACACACGGTGTCTCATGGCTGGCGCGCATCC 2398
2754 QY TGGCGTCAAGCGAGATGCCCGCTTGGAGACTTTTATGGCAGAGTTCGAGTGACA 2813
2399 Db TGAAGCAGGAGGACAACCCCTTCTCTGGAGAACTTTGTAGACACCGTCCGCGACACC 2458
2814 QY ACTGTGCGCCATCTTGCAGCTGTGTGCTGCTAAACATCTCTCTTTCCCGAGCAATGTG 2873
2459 Db ACCGCGCGCACAGGCTCTGCTGTGTGGCCAGAAACGTCGACTGTTTCCGCAAAACAG 2518
2874 QY GAGCAATTTTCTAGGGCAACAATTGATGTGTGGTATTTGTCATGATGGGGGATGCTT 2933
2519 Db GAGCGCTTCGGCGGGGGCCACATCGACGTGTGTGATCGTGCACGCGGCGATGCTC 2578
2934 QY ATGCTACTACCATTCCTACTGAAACAGCAGCAAGGTGTGGCGGAAGTGCAGCATACGGATC 2993

2579 Db ATGCTGTGCCCTTCTCTGCTGGCCAGCACAAAGGTGTGGAGNAAGTGCAGATGCGTATC 2638
2994 QY TTCACAGTAGCCCAATTAGAAGACAAAGTATCCAATTAAGAAGAGGACCTTAGCCACTTC 3053
2639 Db TTCACCGTGGCCAGGTGGACGACAAAGCATCCAGATGAAGAAGAGGACCTGCAGATGTTT 2698
3054 QY CTATATCACTTACGATTTAGCGCGGAGGTAGAGTGGTGGAGATGCATGACAGTATATA 3113
2699 Db TTGTATCACTTGGCGATCAGCGCCGAGGTGGAGTGGTGGAGATGGTTGAAAACGACATA 2758
3114 QY TCAGCATATACTTACGAGCGCACTTTGATGATGGAACAAAGTCCACAGTCTTCGGCAC 3173
2759 Db TCTGCTTTCACCTAGCAGAGGACACTAATGATGGAGCAGAGTCCAGATGCTGAAGCAG 2818
3174 QY ATGCGGCTATCCAAAACAGAGCGAGACAGAGGACCAATTTGGTGAAGAGCCGAAACTCA 3233
2819 Db ATGACGTGTCTCAAGAACGAGCAGGAGCGAGGCGCCAGCTGATCCACGACAGGAACACC 2878
3234 QY ATGTACGATTGACGAGCATTTGGCTCTGATGAGGACGAAGAGACAGAAACCTATCAGGAG 3293
2879 Db GC-----GTCCACACCGCGCGCGCAGCCAGGACCCAAAGCGCCGCTACGCCAGAC 2929
3294 QY AAGGTGCACATGACTTGGACAAAGACAAAGTACATGSCATCCCGG---GGACAAAAGCG 3350
2930 Db AAGGTGCAGATGACTTGGACCGAGGAGGAGGAGGAGTGTGCTGAGAAAGTACAGGAGCAGAC 2989
3351 QY AAGTCAATGGAAGGATTCAGGACCTGTTAAACATGCGTCCGGACAGTCCCAATGTGAGG 3410
2990 Db ACCAGCTTATCCGGTTTCAAGAGCTCTTTCAGCATGAAGCCGACCACTCCAACGTGAGG 3049
3411 QY CGGATGCATCAGCAGTGAATACTCAACAGAGTTTATAGTTAAAGTCCATGAAAGCAAG 3470
3050 Db CGGATGCACAGGCTGTGAAGCTCAATGGCTGCTGTCNTCAACAGTCCAGGATCGCGAG 3109
3471 QY CTGTTTTTATTGAATATGCCAGGGCCACCCCGAACCTTGAGGGTGTGTAAGAACTACATG 3530
3110 Db CTGTCCTGCTCAACATGCCAGGTCCTCCCAAAACCGGAGGGAGACGAGAACTACATG 3169
3531 QY GAGTTCCTTAGAGTGTCTTACCGAGGAGCTAGAGCGAGTCTTACTTGTCCGGGGTGGTGGC 3590
3170 Db GAGTTTCTTGAAGTCTGACCGAGGGCTGAACAGAGTCTCTCTCGTTCAGGGGTGGCGGC 3229
3591 QY AGTGAAGTATCACAATTTATTATAA 3617
3230 Db CGGAGGTGATCACCATCTACTCTATA 3256

RESULT 8

US-09-835-976B-13
; Sequence 13, Application US/09835976B
; Publication No. US20030027983A1

GENERAL INFORMATION:

; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND
; FILE REFERENCE: Attorney docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 5155

; TYPE: DNA

; ORGANISM: mouse

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (73)..(3321)

; FEATURE:

Qy		1168	TGGCGCTGATGTGAACAGTTTGGCCTCANTTTTCTGGCCTGTGTCAITGTCTGCCA	1222
Db		875	TTGGTGCAAATATGTCAACAGCTGGCACTGGTCTTCCTTAGCCGTGTGTGCTTTCTA	934
Qy		1228	TCFTTGGCCACTATGTGTGGAGCCATCAAGTCTCTTTTGTCTCTCCACACTTCCC GGCTCT	1287
Db		935	TCCTGGCATCTATGTGTGTGTCTACAAGACGCCTTTGGCCCCACCTGACATCCCGGTCT	994
Qy		1288	GCATGTCTGGGTAAACCGCACTCTTTTTCATCAAGACACATTGACGTTTGTCTTAAGACCAAGG	1347
Db		995	GCCTTCTAGGGAACCGCACGCTGGCAATTCGCAACTTTTGATACCTGTGTGCGCAAGATGCAGG	1054
Qy		1348	AAATTAACAACATGACAGTCGCCCATCAAA GTTATGGGAGTTCTCTGTAACTCAGTCAAT	1407
Db		1055	TTGTCAAGCAACGGTACAGTGACCACCTGC ACTCTGGGGCCCTCTTCTCGCAATG---GCTCCA	1111
Qy		1408	TTTTTCAATGCCACTGTGATGAATACTTTTGTTCACAATAACGTCAC TTCAATCCAGGGCA	1467
Db		1112	GCCTTGGGTGCCACTGTGATGAGTACTTTTG CACAGAACAACGTTACTTGAGATACAGGGCA	1171
Qy		1468	TTCTCTGGATTGGCTAGTGGTATTAATTAC AGAGAATCTTTGGAGTAATTACTTACCACCAAGG	1527
Db		1172	TCCTGGTGTGGCCAGTGGTGTCTTCTCTGG ATAACCTGTGGAGCACATAATTCAGACAAAGG	1231
Qy		1528	GAGAGATATCGAAAA-----GCCTTCAGC CAANAUTCTTCTGATGTCTTTAGGCAGCT	1578
Db		1232	GGGCAITTTGTGAAAAGAAAGGTGTGTCTCT CAGTGGCTGTGTCGAGGAGAGCGGCGCTG	1291
Qy		1579	TAAACNATGAATATGTCTTGTGTGACATCA CACACCTCTTTCAGCCTTCTGTGGTGGGAATCT	1638
Db		1292	GTGGATTGCCATACGTCCTCACAGACATCAT GACCACTTTCACCATGCTAGTTGGGCATCT	1351
Qy		1639	TCCTTTCCTCTGTTTACAGGTATCATGGCTG EATCAAACAGATCTGGAGATCTCGAAAGATG	1698
Db		1352	ACTTCCGCTCTGTAACTGGGATCATGGCAGE ATCAAACGCTCCGGGGACCTCAAGACG	1411
Qy		1699	CTCAGAAGTCTATTCCGATTTGGTACTATCT CTGCCATCTCGACACACTCTCTTTGTTTATT	1758
Db		1412	CCCAGAACTATTCCAAACAGGAGACCAATCT CGGCCATCGTGACTACATCTTTTCATTTATN	1471
Qy		1759	TAGCAATGTTGTCTTTTTTGGTGATGTATTG AAGGGTGTTCACAGAGACAAAGTTG	1818
Db		1472	TTTCTCTGCATAGTGTCTTTTGGGGCCCTG CAAATGAAAGTGTAGTCTCGCGAGATAAGTTG	1531
Qy		1819	GTGATGCTGTGAAAGGTAAATTTGGTGGTAG GCACCTTATCTGGCCATCCCCATGGGTGA	1878
Db		1532	GGHAGGCTTGCBAAGGAACTGGTCATTGGCA TGTGGCTGGCCATCTCCCTGGGTCA	1591
Qy		1879	TTGTATTGGCTCCTCTCTTTTCAACATGTGG GCTGGACTTCAGAGCCTCACAGGTGCAC	1938
Db		1592	TTGTGATTGGCTCCTTCTTCTCACCTGTGGT GTGTGGCTTCGAGAGCCTGACTGGGGCAC	1651
Qy		1939	CGAGGTGCTCAAGCTATTTCGCAAGGATAAC ATCATACCGTTTCTGAGGGTTTTGGCC	1998
Db		1652	CCCGCCTTACTTCGAGGCCATTTCGCGGTGTG CAGGGAATCATCCCTCTTCTACAGGTGTGTC	1711
Qy		1999	ACAGCAAGCAATGGGGAACTTACCTGGGCTTT TACTTCTAACTGTCTGCCATGTCACAGC	2058
Db		1712	ATGGAAGGCCAACGGGGAGCCACATGGGCCCT TGCTCTACGCGTCTCATCTGTGAGA	1771
Qy		2059	TTGGAATACTCATTTGCCCTCCCTGGATCTTG TGCCGCCAAATCTTTTTCATGTTTTTCTCA	2118
Db		1772	CCGGTATCCTCATCGCCTCCCTGGACAGTGTG GCGCCCCCATCTGTCTCATGTTCTTCNTCA	1831
Qy		2119	TGTGTTTACCTCTTTGTAAACTTGTGCATGTGC CTTGTGAAAACATTACTTTCGAACACCCCACT	2178
Db		1832	TGTGCTACATGTTTGTCAATCTGGCCTGTGCG GTACAGACCCCTGCTACGCACACCCCACT	1891
Qy		2179	GGAGACCCGATTCGGCTACTACCATTTGGGCC CTTCTTCTTCATGGGAATGAGTATCTGTC	2238
Db		1892	GGCGTCCACGGCTTCAAGTTCTACCACTGGAC CCCTCTCTCTTCTTGGGATGAGTCTCTGCC	1951
Qy		2239	TGGCTCTGATGTTTCATTTCTTCTCTGGTATT ATATGCAATGTAGCCATGGTATAGCTGGTA	2298

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Db 1952 TCGCGCTGATGTTTCATCTGCTCTCTGTACTACGCCNTTTTGGCCATGCTCATTTGCCGGCT 2011
Qy 2299 TGATCTACAAGTACATGTAATACCAAGAGCTGAGAAAGAATGGGGTGATGGTATCCGTTG 2358
Db 2012 GCATCTTACAAGTACATCGAGTACCGCGGGCTGAGAAGAGTGGGGGATGTCATCAGG 2071
Qy 2359 GGCTGCTCCCTCAGTCAGCCCGGTTTGGCTTTCGATTTGAGAGAGACCTCCACACA 2418
Db 2072 GCTGTGCTACTGAATGCTGCCCCCTACGCCCTCTGCGTGTGAAACAATGGGGCCCCACATA 2131
Qy 2419 CTAATAAATCGAGGGCTCAGTTGCTTGTATTACTGAAACTAGATGAAGACTTTACATGTCA 2478
Db 2132 CCAAGACTGAGGCCCCAGGTGTTGGTGTGATGCTGAACTGACCTCGAGAGAGTGTGTA 2191
Qy 2479 AGCATCTCGCTCTCTCACCCTTGGCTCACAGCTCAAGCAGGAAAGGTNTCACTATTG 2538
Db 2192 AGCACCCCCCGCTGTCTCTTCACTCTCAGCTGAAGGCTGGCAAGGSCCTGACCATCG 2251
Qy 2539 TGGGCTCTGTCTATCGTGGGGAATCTCTAGAGAACTACGGTGAAGCTTTAGCTGTGAGC 2598
Db 2252 TGGGATCTGTGTAGAGGACCTACTTTAGACAAGCATGTGAGAGGCCAGAGGGCTGAAG 2311
Qy 2599 AGACCATAAAGCACCTAATGGAGGAGAGAAAGGATTTCTGCCAGCTGGTGG 2658
Db 2312 AGAATATCCGGTCTCTGATGAGTCAGAGAGACGAGGGCTTCTGCCAGCTGGTGGTGT 2371
Qy 2659 CGCCAAAGCTGAGAGGGGCAATTTCCCACTCATCCAGTCATGTGGCCCTTGGGGGCATGA 2718
Db 2372 CCTCAACCTCGAGATGGTGGTCCCACTCATCCAGTCGCTGGCTCGTGGCATGA 2431
Qy 2719 AGCAACAACCGTGTGATGGCTGGCTTAATGGCTGGGCTCAAAAGGAAAGATGCCCGG 2778
Db 2432 AACACAACACTGTCTCTATGGCTGGCCAGAGGCTTGAAGAGGAGCAGATATCTTTCT 2491
Qy 2779 CTGGAAGACTTTTATGSCAGTTCGAGTGACAACTGCTGCCCTCTTGCACTGCTGG 2838
Db 2492 CCTGGAAGAACTTTGTAGACACAGTCGCTGGTACACTACAGACACATCAGGCTTGTGG 2551
Qy 2839 TGGCTAAACAACTCTCTTTCCAGCAATGTGGGCAATTTTCTGAGGGCAACATTTG 2898
Db 2552 TGGCCAAGAACATTGACTTATTTCCCAACAAACCAAGAGGCTTCAGCGAGGGAACATTTG 2611
Qy 2899 ATGTGTGTGATTTGTGATGATGGGGATGCTTATGCTACTACATTCCTACTGAAAC 2958
Db 2612 ATGTGTGTGATGCTGATGATGACGGGGCATGCTCATGCTTCTGCCCTTTCTGTGCGCC 2671
Qy 2959 AGCAAAAGTGTGGGAAAGTGACAGTACAGTACGATCTTCACAGTAGCCCAATTAGAGACA 3018
Db 2672 AGCAAAAGTGTGGGAAAGTGCCGATGCGCATCTTCACTGTGGCCAGGTGGATGATA 2731
Qy 3019 ACAGTATCCAAATGAAGAGACCTTAGCCACCTTCTTATCATCTTACCTTATGAGGCGG 3078
Db 2732 ACAGCATCCAGTGAAGAGGACCTTCGAGATGTTCTGTACCACTCAGGATCAGTGGC 2791
Qy 3079 AGGTAGAAGTGTGAGATGCAATGACAGTATATCAGCATATATCTTACAGCGCACTT 3138
Db 2792 AGGTGAGGTGTGAGATGTTGAAATGATATTTCCGCATTTCACTATGAGAAGACGC 2851
Qy 3139 TGATGATGAAACAAAGTCCAGATGCTTCGGCACATGGCTATCCAAACAGAGCGAG 3198
Db 2852 TAATGATGGAGAGGTCACAGATGCTTGAACAGATCAGTGTGCAAAAGATGAGCGG 2911
Qy 3199 ACAGAGGGCACAATTTGTTGAAGACCCGAAACTCAATGCTACGATTTACCAAGCATTTGCT 3258
Db 2912 AGAGAGAGGCCAGCTGATTCATGACAGGAACATGCACTCCATCCACACGAACCTGCTA 2971
Qy 3259 CTGATGAGGACGAAGAGACAGAAACCTTATCAGGAGAGGTGCACATGCTTTGGACAAAG 3318
Db 2972 GAAACCAAGCCCCACCAACA-----CCGACAAAGTGCAGATGATGATGAGCGAAAG 3022
Qy 3319 ACAAGTACATGGCATCC---CGGGGACAAAGCGAAGTCAATGGAAGGATTCAGGAGCC 3375
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Db 3023 AGAAACTCATTTGCAGAGAAAACACAGGAACAAGGACACTGGGCCCATCAGGCTTCAAAGACC 3082
Qy 3376 TGCTTAAACATCGTCCGGACCACTCAATGTGAGCGGATGCATACAGCAGTGAACACTCA 3435
Db 3083 TCTTCAGCCTAAAGCCGACCACTCAACGTCAGGAGGATGCATACTGCTGTGAAGNTCA 3142
Qy 3436 ACGAGGTATATAGTTTAAACAAGTCCCATGAAGCAAGCTGGTTTTATTGAATATGCCAGGC 3495
Db 3143 ACGGCGTAGTTTCTCAACAAGTCCCAAGATGCCAACTGGTCTGCTGTAATATGCCAGGCC 3202
Qy 3496 CACCCGAAACCTTGAGGGTGATGAAACTACATGAGTTCCTAGAGGTGCTTACCGAGG 3555
Db 3203 CCCCMAAAGTCGGCAGGGGACAGAACTACATGAGTTCCTCAGGTCTTCGACGGAAG 3262
Qy 3556 GACTAGACGAGTCTCTACTTGTCCGGGTGGTGGCAGTGAAGTATCATCCCAATTTATCAT 3615
Db 3263 GGCTGAACAGGGTCTCTCTGTGTCAGGGGTGGTGGCCGAGAGTTCATCACCATCTACTCT 3322
Qy 3616 AAC 3618
Db 3323 AAC 3325
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RESULT 9

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US-09-835-976B-11
; Sequence 11, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3348)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1072)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2746)
; OTHER INFORMATION: n=c or a, Xaa=Leu or Ile
; US-09-835-976B-11
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Query Match 32.7%; Score 1392.4; DB 11; Length 5907;
Best Local Similarity 69.6%; Pred. No. 0;
Matches 1917; Conservative 0; Mismatches 821; Indels 15; Gaps 2;
Qy 483 GACGACATGAAGAGCTCGAAATGCTTATCTCAATTAATTCCAATTATGAAGAGGAGAT 542
Db 55 GATGGCAACCCCAAGGAAAGCAGTCCCTTCATCAACAGCACCGACACAGAGAGGGAAG 114
Qy 543 GAATATTTTGAATAAAATTTGGCACTCTTTGAGGAGAAATGGACACAGACCGAAGGTG 602
Db 115 GAGTATGATGGCAAGAACATGGGCTTGTGTTGAGGAGGAGATGGACACCGCCCTATGGTG 174
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Db 2332 AACTGGCCGAGAGAAAGATCATCAGACGTGGAGAACTTTCATTGAGCTGCTCCGGNA 2391
QY 2811 ACAACTGTGCCCATCTTGCATCTGCTGGTGTAAACATCTCTCTTTCCAGCAAT 2870
Db 2392 ACCACAGCTGGCCACTTAGCCCTCTGCTGGTCAACAAGACGTTTCCATGTTTCTCGGAAC 2451
QY 2871 GTGGAGCAATTTCTGAGGGCAACATTGATGTGGTGAATTTGTCATGATGGGGGATG 2930
Db 2452 CCTGAGCGCTTCTCTGAGGGCAGCATCGACGTTTGGTGAATTTGTCACGATGGAGGCATG 2511
QY 2931 CTTATGCTACTACCATTCCTACTGAAACAGCAAGGTGTGGCAAGTGCAGCATACGG 2990
Db 2512 CTCATGCTGCTGCCCTTCTCTGCTGGCACCACAGAGTCTGGGGAAGTGCAAGTGGT 2571
QY 2991 ATCTTCACAGTAGCCCAATTAGAAGACAAAGTATCCAAATGAAGAGGACCTAGCCACC 3050
Db 2572 ATCTTCACGTGTGCCCAGATGATGACATAGCATCCAGATGAAGAGGATCTGACCACA 2631
QY 3051 TTCTCTATACCTTAGCATTGAGGGGAGGTAGAGTGGTGGAGATGCATCAGATGAT 3110
Db 2632 TTCTCTGATCATTTACGCACTACTCGGAGGTGCGAGGTGGAGATGCATGAGCGGAC 2691
QY 3111 ATATCAGCATATCTTACGAGCGCACTTTGATGATGGAACAAAGTCCAGATGCTTCGG 3170
Db 2692 ATCTCAGCTTACCTATGAGAGAGCTTGGTGTATGGACGCGTTCCCGATGCTCAA 2751
QY 3171 CACATGCGGCTATCCAAACAGAGCGGAGACAGAGAGGCAAAATGGTGAAGA 3223
Db 2752 CAGATGCAATTAACCAAGATGAGCGGAGCGGAGATCCAGATATCACAGA 2804

RESULT 10
US-09-835-976B-110
; Sequence 110, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-835-976B-110

Query Match 17.3%; Score 735; DB 11; Length 807;
Best Local Similarity 100.0%; Pred. No. 5.7e-204;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3526 ACATGGAGTCTAGAGGTGCTTACCGAGGACTAGAGCGACTCTACTTGTCCGGGTG 3585
Db 73 ACATGGAGTCTAGAGGTGCTTACCGAGGACTAGAGCGACTCTACTTGTCCGGGTG 132
QY 3586 GTGGCAGTGAAGTGCATCACTTTATTAACCTACTCTGAATGACCGTGTGACCTG 3645
Db 133 GTGGCAGTGAAGTGCATCACTTTATTAACCTACTCTGAATGACCGTGTGACCTG 192
QY 3646 TTTTCTTAAAGCCCTACTCTCTCCATGAAGTGCAGCTCATTAATCACTCCACCTC 3705
Db 193 TTTTCTTAAAGCCCTACTCTCTCCATGAAGTGCAGCTCATTAATCACTCCACCTC 252
QY 3706 AACTAGAGCCCTGTGTTCTGTACATCATCTACTGACTCTTATGAGCTGAGCCCTCAAGT 3765
Db 253 AACTAGAGCCCTGTGTTCTGTACATCATCTACTGAACTCTTGTGAGCTGAGCCCTCAAGT 312
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QY 3766 ACCTGTGTAAAGAGCTCCCATCTGATCTGCAGTCAATTACAGAAAAACCAATATTTCCT 3825
Db 313 ACCTGTGTAAAGAGCTCCCATCTGATCTGCAGTCAATTACAGAAAAACCAATATTTCCT 372
QY 3826 CAACATCAGAACAAATGCTCAAGTCTTTCAAGCCCACTGTCTGAGCAGTCAAGGCAAAATTA 3885
Db 373 CAACATCAGAACAAATGCTCAAGTCTTTCAAGCCCACTGTCTGAGCAGTCAAGGCAAAATTA 432
QY 3886 GAATTTAAACAAGCTGAGCCAAATAAATGAATTTGGTAAAAGGGATGCTAGAAATTCAACTGAA 3945
Db 433 GAATTTAAACAAGCTGAGCCAAATAAATGAATTTGGTAAAAGGGATGCTAGAAATTCAACTGAA 492
QY 3946 GAAAAAAGCAAGTCAAGTACGTATTGAGCAATTAAGATGAATCTCAGAGTCATGGTTC 4005
Db 493 GAAAAAAGCAAGTCAAGTACGTATTGAGCAATTAAGATGAATCTCAGAGTCATGGTTC 552
QY 4006 AATGTTGACACTGTGAGGATAACAACCTAGACAGCTTTCATCTTACTAAAGAAATTTATGG 4065
Db 553 AATGTTGACACTGTGAGGATAACAACCTAGACAGCTTTCATCTTACTAAAGAAATTTATGG 612
QY 4066 TCAAGTATATTTGGACCTATTATCTCGGCAAGCAAGATGCAACATTTTTAGCTATA 4125
Db 613 TCAAGTATATTTGGACCTATTATCTCGGCAAGCAAGATGCAACATTTTTAGCTATA 672
QY 4126 TTTCTTTAGTATACCCACTGCTGTAATTTTATATTTAGGATATTAACCTTGAACATGGCTG 4185
Db 673 TTTCTTTAGTATACCCACTGCTGTAATTTTATATTTAGGATATTAACCTTGAACATGGCTG 732
QY 4186 CAGCTCTACTTCTTCAAAAACATCCCCCAAAATACCAGATTTAAATATCCAAAAAAA 4245
Db 733 CAGCTCTACTTCTTCAAAAACATCCCCCAAAATACCAGATTTAAATATCCAAAAAAA 792
QY 4246 AAAAAAATAAAAAA 4260
Db 793 AAAAAAATAAAAAA 807
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RESULT 11

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US-09-835-976B-112
; Sequence 112, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: n=a, c, g, or t
US-09-835-976B-112
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Query Match 14.4%; Score 613.4; DB 11; Length 2290;
Best Local Similarity 73.0%; Pred. No. 5.3e-168;
Matches 788; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

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QY 2538 GTGGCTCTGTCATCGGGGAACCTCCTAGAGAACTACGGTGAAGCTTTAGCTGCTGAG 2597
Db 7 GAGGACAGACTCTTCTGGGAGACTACCTAGACAGCCATGACAGATCACAGCAGAG 66
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QY 2598 CAGACCATTAAGCACCTTAATGAGGCGAGAAAGGATTTCTGCCAGCTGGTGTG 2657
Db |||||
67 CAGGCACTGAAACACTTAATGAAACAAGTAAAGGCTTTTGCCAACTGGTTGTG 126
QY 2658 GCGGCCAAGCTGAGAGAGGCAATTTCCACCTCATCCAGTCATGTGGCTTGGGGGATG 2717
Db |||||
127 GCTCAGAAGTTGAAAGAGGCGCTTTTCCATCTTATACAGTCTGTGGTCTTGAGGAATG 186
QY 2718 AAGCAACAACCGGTGGTGGCTGGCTTAATGGCTGCGTCAAGGGAAGATCCCGC 2777
Db |||||
187 AGGCATACACCTGTAATCATAGCTGGCCAAAGTAGCTGGAGACAGATGATCACTACGG 246
QY 2778 GCTTGGAACTTTTATTTGGACAGTTCGAGTGACAACCTGCTGCCCATCTTTCACCTGCTG 2837
Db |||||
247 GCTTGGAACTTTTATTTACTACTACCTATGCTGTGACCAAGCTGCAGGCCAAGCACTTCTG 306
QY 2838 GTGGCTTAAACATCTCTCTTTTCCAGCAATGTGGAGCAATTTTCTGAGGGCAACATT 2897
Db |||||
307 GTAGCAAGAATGTATCTCTTTTCCCTGGCTCCCGTGAAACATTAGCAGAAGGCGACATT 366
QY 2898 GATGTGTGTGATGTGCATGATGGGGGATGCTTATGCTACTACCATTTCTACTGAAA 2957
Db |||||
367 GATGTTTGTGTGATGATGATGAGGGGCAATGCTTATGCTTCTGCGCTTCTCTTAAAA 426
QY 2958 CAGCAACAGGTGTGGCGAAGTGCAGCATACGATCTTCCACAGTAGCCCAATTAGAAGAC 3017
Db |||||
427 CAACAACAGGTGTGGAGGAAGTGAAGATGCGTATTTTTCACGTGGCTCAGATGGAAGAC 486
QY 3018 AACAGTATCCAAATGAAGAGACCTTAGCCACTTCTTATATCATCTTACGATTTGAGGG 3077
Db |||||
487 AACAGTATTTCAAATGAAAGAGACTTTGGCTAGCTTTCTTTATCATTTTACGTATCGTGT 546
QY 3078 GAGGTAGAGTGTGAGATGCATGACAGTGATATATCAGCATATATACGAGCGCACT 3137
Db |||||
547 GATGTGAGTGTGAGATGCATGACAGTGATATATCAGCATATATCAGCATATGAAAGCACA 606
QY 3138 TTGATGATGAAACAAAGTCTCCAGATGCTTCGGCAGATCGCGCTATCCAAAACAGAGCGA 3197
Db |||||
607 CTCATGATGAGCAGAGATCAAAATGCTGAGACAAATCGCTTTCTTAAACAGATCGG 666
QY 3198 GACAGAGGCAATTTGTGAAAGCCGAACTCAATGCTACGATTTGACAGCATTTGGC 3257
Db |||||
667 GAGCGAGAGGCTCAGTTGGTGAAGGACAGGAATTCATCTCGCTTTTACCAAGTGTGGGC 726
QY 3258 TCTGATGAGGACGAGAGACAGAACTTATCAGGAGAGGTGCATGATCTTGGACAAA 3317
Db |||||
727 TCTGATGATGATGAGATACAGAGGCTGCCAGAGAGATGATATGATCTTGGACAGG 786
QY 3318 GACAGATACATGGCATCCCGGGGACAAAAGCGAAGTCAATGGAAGGATTCAGGACCTG 3377
Db |||||
787 GACAGCACCATGCACTCGTGTGTCGCCAAAGCAACCAATGCCGAGCTGTCCAGACCTC 846
QY 3378 CTTAATCATCGTCCGACAGCTCCAAATGTGAGCGGATGCATACAGCAGTGAACCTCAAC 3437
Db |||||
847 CTTAATCATACGACCGACAGCTCAAAATGTTCGCGGTATGCACACAGCTGTGAAACTTAAT 906
QY 3438 GAGGTTATAGTTAAACAAGTCCATGAAGCAAAAGCTGTTTTTATGATATGCCAGGCCA 3497
Db |||||
907 GAAGTCATTTGAATTAATCCCATGATGCCAACTGGTTTTGCTCAACATGCCAGACCC 966
QY 3498 CCCCAGAACCTCGAGGATGATAAACTACATGAGTTCCTAGAGTGTCTTACCGAGGGA 3557
Db |||||
967 CTTGTAACCTTCAGGCTGATGAAATTTATATGAGTTTCTAGAGTTCTGACAGAGGGC 1026
QY 3558 CTAGACGAGTCTACTTGTCCGGGTGTGGCAGTGAAGTATCACCATTTTATTCATA 3616
Db |||||
1027 TTGAGCGGTGTGCTGTGTAGTGAGAGAGGTGGAACAGAGGTGATCATCACTTTACTCGTA 1085
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RESULT 12

US-09-918-995-9696
; Sequence 9696, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9696

; LENGTH: 478

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(478)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-9696

Query Match 10.5%; Score 446.4; DB 11; Length 478;

Best Local Similarity 99.6%; Pred. No. 1.4e-119;

Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2403 GAAGGACCTCCACACACTTAAAGGCTGAGGCTCAGTTGCTTGTATTACTGAAACTAGAT 2462

Db 30 GAACGACCTCCACACACTTAAAGGCTGAGGCTCAGTTGCTTGTATTACTGAAACTAGAT 89

QY 2463 GAAGACTTTACATGTCAAGCATCTCGCTCTCTACCTTTGGCTCACAGCTCAAGCAGGA 2522

Db 90 GAAGACTTTACATGTCAAGCATCTCGCTCTCTACCTTTGGCTCACAGCTCAAGCAGGA 149

QY 2523 AAAGTNTCACTATTGCGGCTCTGTCTATCGTGGGAACTTCTTAGAGAACTACCGTGAA 2582

Db 150 AAAGTCTCACTATTGCGGCTCTGTCTATCGTGGGAACTTCTTAGAGAACTACCGTGAA 209

QY 2583 GCTTTAGCTGTGAGCAGACCATAAAGCACCTTAATGGAGGAGAGAGGTAAGGATTC 2642

Db 210 GCTTTAGCTGTGAGCAGACCATAAAGCACCTTAATGGAGGAGAGAGGTAAGGATTC 269

QY 2643 TGCCAGCTGTGTGGCGCCCAAGCTGAGAGAGGCAATTTCCACCTCATCCAGTCATGT 2702

Db 270 TGCCAGCTGTGTGGCGCCCAAGCTGAGAGAGGCAATTTCCACCTCATCCAGTCATGT 329

QY 2703 GGCCTTGGGCGATGAAGCACAACACGCTGTGATGGCTGGCTTAATGGCTGGCGTCAA 2762

Db 330 GGCCTTGGGCGATGAAGCACAACACGCTGTGATGGCTGGCTTAATGGCTGGCGTCAA 389

QY 2763 AGCGAAGATGCCGGCTTTGGAAGACTTTTATTTGGCAGAGTTCGAGTGACAACCTGCTGCC 2822

Db 390 AGCGAAGATGCCGGCTTTGGAAGACTTTTATTTGGCAGAGTTCGAGTGACAACCTGCTGCC 449

QY 2823 CATCTTGCACTGCTGTGGCTTAAACAT 2851

Db 450 CATCTTGCACTGCTGTGGCTTAAACAT 478

RESULT 13

US-09-976B-84

; Sequence 84, Application US/09835976B

; Publication No. US20030027983A1

; GENERAL INFORMATION:

; APPLICANT: Mount, David B.

; APPLICANT: Delpire, Eric

; APPLICANT: Gamba, Gerardo

; APPLICANT: Alfred L. George, Jr.

; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC ACID

; TITLE OF INVENTION: POLYPEPTIDES AND

; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2

; CURRENT APPLICATION NUMBER: US/09/835,976B

; CURRENT FILING DATE: 2001-04-16

Db 197 CTTATGGTATTAGTGGTATTATTCGGCGTACGCTATGTGAACAAGTTTGCCTCACTTTTC 256
 Qy 1206 CTGGCCTGTGTCATTGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTT 1265
 Db 257 CTGGCCTGTGTCATTGTGTCCATCTTGGCCATCTATGCTGGAGCCATCAAGTCTTCTTTT 316
 Qy 1266 GCTCCTCCACACTTCCCG 1283
 Db 317 GCTCCTCCACACTTCCCG 334

Search completed: November 27, 2003, 01:01:31
 Job time : 1236 secs